



P07741US01_6-19-06_Sequence.txt
SEQUENCE LISTING

<110> BRUCK, Magnus

<120> BIOINFORMATIC METHOD FOR IDENTIFYING SURFACE-ANCHORED PROTEINS
FROM GRAM-POSITIVE BACTERIA

<130> P07741US01/BAS

<140> 10/661809

<141> 2003-09-15

<150> 60/410303

<151> 2002-09-13

<160> 57

<170> PatentIn version 3.1

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<212> PRT

<213> Staphylococcus epidermidis

<220>

<221> MISC_FEATURE

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<211> 777

<212> PRT

<213> Staphylococcus epidermidis

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Gly Ala Ile Val Ser Ile Glu Lys Ala Glu Lys Asn Phe Val Ile Thr
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Tyr Ala Ser Gly Lys Lys Ala Gln Ile Ser Ile Leu Asn Asp His Leu
Page 1

35

40

45

Phe Arg Tyr His Leu Asp Pro Thr Gly Lys Phe Glu Glu Tyr Pro Thr
50 55 60

Pro Asn Asp Pro Lys His Val Ala Lys Ile Thr Ala Lys Thr Met Ala
65 70 75 80

Asp Tyr Gly Thr Gln Ala Phe Glu Gln Thr Asn Val Thr Asp Ser Gly
85 90 95

Asn Gln Phe Ile Leu Glu Asn Asn Gly Leu Lys Ile Met Phe Glu Lys
100 105 110

Glu Ser Ala Leu Met Lys Val Leu Asp Lys Lys Lys Asn Gln Val Ile
115 120 125

Leu Glu Glu Thr Ala Pro Leu Ser Phe Lys Asn Asp Lys Ala Thr Gln
130 135 140

Thr Leu Lys Gln Ser Ser Gln Glu Asn Tyr Phe Gly Gly Gly Thr Gln
145 150 155 160

Asn Gly Arg Phe Thr His Lys Gly Thr Ala Ile Gln Ile Val Asn Thr
165 170 175

Asn Asn Trp Val Asp Gly Gly Val Ala Ser Pro Asn Pro Phe Tyr Trp
180 185 190

Ser Thr Ala Gly Tyr Gly Val Val Arg Asn Thr Trp Lys Pro Gly Asn
195 200 205

Tyr Asp Phe Gly Ser His Asp Pro Gln Lys Thr Thr Thr Thr His Glu
210 215 220

Gly Thr Asp Phe Asp Ala Phe Tyr Phe Phe Asn Asp Ser Ser Ala Gly
225 230 235 240

Ile Leu Lys Asp Tyr Tyr Glu Leu Thr Gly Lys Pro Ala Leu Met Pro
Page 2

Glu Tyr Gly Phe Tyr Glu Ala His Leu Asn Ala Tyr Asn Arg Asp Tyr
260 265 270

Trp Val Lys Val Ala Glu Gly Thr Ala Gly Ala Val Lys Phe Glu Asp
275 280 285

Gly Asn Phe Tyr Lys Glu Tyr Gln Pro Gly Asp Leu Gly Asn Leu Asn
290 295 300

Gly Thr Leu Glu Ser Leu Asn Gly Glu Lys Glu Asn Tyr Gln Phe Ser
305 310 315 320

Ala Arg Ala Val Ile Asp Arg Tyr Lys Lys Asn Asp Met Pro Leu Gly
325 330 335

Trp Phe Leu Pro Asn Asp Gly Tyr Gly Ala Gly Tyr Gly Gln Thr Asp
340 345 350

Ser Leu Asp Gly Asp Val Gln Asn Leu Lys Glu Phe Thr Glu Tyr Ala
355 360 365

Gln Ala Asn Gly Val Glu Val Gly Leu Trp Thr Gln Ser Asn Leu His
370 375 380

Pro Ala Asp Pro Lys Asn Pro Lys Lys Gly Glu Arg Asp Ile Ala Lys
385 390 395 400

Glu Val Ser Val Ala Gly Val Lys Ala Leu Lys Thr Asp Val Ala Trp
405 410 415

Val Gly Tyr Gly Tyr Ser Phe Gly Leu Asn Gly Val Glu Asp Ala Ala
420 425 430

Asn Val Phe Val Lys Glu Thr Asp Gly Ala Val Arg Pro Met Ile Val
435 440 445

Ser Leu Asp Gly Trp Ala Gly Thr Gln Arg His Ala Gly Ile Trp Thr
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450

455

460

Gly Asp Gln Thr Gly Gly Gln Trp Glu Tyr Ile Arg Phe His Ile Pro
465 470 475 480

Thr Tyr Ile Gly Thr Ser Leu Ser Gly Gln Pro Asn Val Gly Ser Asp
485 490 495

Met Asp Gly Ile Phe Gly Gly Lys Asn Lys Glu Ile Asn Ile Arg Asp
500 505 510

Phe Gln Trp Lys Thr Phe Thr Pro Val Gln Leu Asn Met Asp Gly Trp
515 520 525

Gly Ser Asn Pro Lys Thr Pro Phe Ala Phe Asp Gln Glu Ala Thr Asp
530 535 540

Leu Asn Arg Ala Tyr Leu Lys Leu Lys Ser Met Met Met Pro Tyr Asn
545 550 555 560

Tyr Ser Ile Ala Lys Glu Ser Val Asp Gly Leu Pro Met Val Arg Ala
565 570 575

Met Ala Leu Glu Phe Pro Asn Glu Gly Thr Ala Tyr Thr Lys Asp Ser
580 585 590

Gln Tyr Gln Tyr Met Trp Gly Pro Asn Leu Leu Val Ala Pro Ile Tyr
595 600 605

Asn Gly Asn Gln Asp Glu Ala Gly Asn Ser Ile Arg Asp Gly Ile Tyr
610 615 620

Leu Pro Asp Glu Lys Gln Val Trp Val Asp Leu Phe Thr Gly Glu Lys
625 630 635 640

Tyr Gln Gly Gly Arg Val Leu Asn Gly Val Lys Thr Pro Leu Trp Lys
645 650 655

Val Pro Val Phe Val Lys Asp Gly Ser Ile Ile Pro Met Thr Asn Pro
Page 4

660

665

670

Asn Asn Asn Pro Lys Glu Ile Gln Arg Asp Gln Arg Ser Phe Leu Ile
 675 680 685

Tyr Pro Asn Gly Thr Thr Ser Phe Asn Met Tyr Glu Asp Asp Gly Ile
 690 695 700

Ser Thr Ser Tyr Glu Ala Gly Gln Ser Ala Thr Thr Lys Ile Asn Ser
 705 710 715 720

Gln Gly Pro Lys Ser Asn Glu Lys Gly Asp Leu Thr Val Thr Ile Glu
 725 730 735

Pro Thr Lys Gly Ser Tyr Lys Asp Phe Val Asp Glu Arg Ser Thr Thr
 740 745 750

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Gly Gly Thr Glu Val Thr Leu Lys Gln
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<211> 1010

<212> PRT

<213> Staphylococcus epidermidis

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 20 25 30

Lys Leu Asn Gln Ser Ala Leu Ser Val Lys Leu Ala Lys Gln Ser Val
 35 40 45

Thr Ala Lys Asp Val Gln Ile Thr Val Lys Gly Phe Ile Asn Lys Gly
 50 55 60

P07741US01_6-19-06_Sequence.txt

Thr Val Asp Gly Gly Asn Thr Thr Val Asp Asp Gln Leu Thr Ile Pro
65 70 75 80

Ala Asn Val Ala Ile Asn Glu Glu Lys Thr Thr Pro Ser Ser Leu Thr
85 90 95

Leu Gln Trp Asp Gln Val Thr Glu Ala Thr Ser Tyr Glu Val Glu Arg
100 105 110

Asp Gly Thr Val Phe Gly Asn Ile Gln Thr Asn Thr Ala Thr Phe Asp
115 120 125

Gly Phe Ser Phe Leu Ser Glu His Thr Phe Arg Val Arg Ala Val Gly
130 135 140

Lys Asn Gly Val Ser Glu Trp Ser Glu Pro Ile Lys Gly Lys Thr Gln
145 150 155 160

Asp Asp Pro Tyr Lys Glu Thr Ile Asn Gln Val Lys Ala Thr Ser Asn
165 170 175

Leu Pro Glu Gln Pro Gly Ala Glu Leu Lys Lys Leu Thr Asp Lys Asp
180 185 190

Leu Ser Thr Gly Trp His Thr Asn Trp Ser Thr Gly Ile Ala Asn Pro
195 200 205

Ser Asp Gly Asn Phe Leu Ser Leu Lys Phe Asp Leu Gly Ala Glu Tyr
210 215 220

Gln Met Asp Lys Ile Glu Tyr Leu Pro Arg Asp Asn Ala Gly Asn Gly
225 230 235 240

Asn Ile Leu Gln Leu Gln Tyr Arg Thr Ser Lys Asp Gly Ala Asn Trp
245 250 255

Thr Glu Phe Ser Glu Pro Ile Asn Trp Lys Gln Asp Ala Leu Thr Lys
260 265 270

P07741US01_6-19-06_Sequence.txt

Thr Ile Glu Thr Lys Asp Gln Ala Tyr Arg Phe Val Glu Met Lys Val
275 280 285

Leu Lys Ser Val Gly Asn Phe Gly Ser Gly Arg Glu Met Leu Phe Tyr
290 295 300

Lys Gln Pro Gly Thr Glu Gly Ile Leu His Gly Asp Ile Thr Asn Asp
305 310 315 320

Gly Thr Ile Asp Glu Asn Asp Ala Met Ser Tyr Arg Asn Tyr Thr Gly
325 330 335

Leu Glu Ser Val Asp Ser Asp Phe Asn Gly Tyr Val Glu Lys Gly Asp
340 345 350

Leu Asn Lys Asn Gly Val Ile Asp Ala Tyr Asp Ile Ser Tyr Val Leu
355 360 365

Arg Gln Leu Asp Gly Gly Ile Glu Ile Pro Asp Val Glu Glu Ile Ala
370 375 380

Gly Gly Leu Ser Leu Ala Val Val Asn Glu Asn Gly Lys Asp Thr Tyr
385 390 395 400

Leu Pro Gly Asp Thr Leu Thr Phe Ile Leu Lys Gly Gln Asp Leu Lys
405 410 415

Asn Ile Asn Ala Leu Ser Thr Lys Met Ser Phe Asp Ser Ser Lys Phe
420 425 430

Glu Leu Val Gly Gln Pro Ala Thr Thr Asn Asn Thr Gln Gln Met Glu
435 440 445

Asn Tyr Ser Lys Tyr Arg Lys His Ser Asn Asp Val Glu Asn Leu Tyr
450 455 460

Leu Val Leu Ser Asn Gln Gly Asn Lys Gln Leu Leu Asn Gly Ser Met
465 470 475 480

P07741US01_6-19-06_Sequence.txt

Asp Leu Val Thr Phe Lys Val Lys Val Lys Glu Thr Thr Arg Val Lys
485 490 495

Arg Ala Thr Thr Val Glu Gln Pro Leu Gln Phe Asp Met Ser Gln Gly
500 505 510

Leu Leu Val Gly Gln Gly Phe Gln Gln Ala Thr Leu Ser Asp Phe Ser
515 520 525

Val Thr Val Lys Pro Thr Glu Leu Val Asp Lys Glu Leu Leu Gln Ala
530 535 540

Leu Ile Thr Leu Asn Gln Ala Arg Val Glu Lys Glu Tyr Thr Pro Glu
545 550 555 560

Thr Trp Ala Ile Phe Lys Pro Ile Leu Asp Glu Ala Val Ala Val Leu
565 570 575

Ala Asn Glu Gln Ala Thr Gln Thr Asp Val Ser Ala Ala Ala Glu Asn
580 585 590

Leu Glu Lys Ala Ala Ser Gln Leu Glu Lys Met Pro Asp Val Ala Asn
595 600 605

Lys Ala Asp Leu Glu Lys Ala Ile Gln Glu Gly Leu Ala Lys Lys Pro
610 615 620

Ser Asp Gly Gln Glu Phe Thr Glu Glu Thr Lys Lys Val Leu Glu Glu
625 630 635 640

Ser Leu Ala Ala Ala Gln Lys Val Phe Ala Gln Glu Lys Val Thr Gln
645 650 655

Glu Glu Ile Asp Gln Ala Thr Lys Thr Leu Arg Glu Ala Ile Ala Gln
660 665 670

Leu Lys Glu Gln Pro Val Ala Val Asp Lys Glu Thr Leu Lys Glu Gln
675 680 685

P07741US01_6-19-06_Sequence.txt

Ile Ala Gln Ala Arg Gly Arg Lys Pro Glu Glu Gly Tyr Gln Phe Thr
690 695 700

Lys Glu Thr Glu Lys Gln Leu Gln Glu Ala Ile Gln Ala Ala Glu Ala
705 710 715 720

Ile Val Ala Lys Glu Thr Ala Thr Lys Glu Glu Val Ser Glu Ala Leu
725 730 735

Asn Ala Leu Glu Thr Ala Met Ala Gln Leu Lys Glu Val Pro Leu Val
740 745 750

Asn Lys Asp Gln Leu Gln Glu Val Val Lys Arg Ala Gln Gln Val Thr
755 760 765

Pro Ser Glu Gly His Gln Phe Thr Ala Ser Ser Leu Gln Glu Leu Gln
770 775 780

Lys Ala Leu Leu Ala Ala Lys Asn Thr Leu Lys Asn Pro Ala Ala Asn
785 790 795 800

Gln Lys Met Ile Asp Glu Ala Val Ala Glu Leu Thr Ser Ala Ile Asp
805 810 815

Gly Leu Gln Glu Glu Val Leu Val Thr Asp Lys Lys Ala Leu Glu Ala
820 825 830

Met Ile Ala Lys Ala Lys Ala Ile Lys Pro Ser Ala Gly Lys Glu Phe
835 840 845

Thr Ser Glu Ser Lys Ala Arg Leu Thr Glu Ala Ile Asp Gln Ala Glu
850 855 860

Gly Ile Leu Ala Asp Lys Asn Ala Arg Gln Glu Gln Ile Asp Ile Ala
865 870 875 880

Glu Lys Asn Val Lys Thr Ala Leu Asp Ser Leu Glu Glu Gln Val Leu
885 890 895

P07741US01_6-19-06_Sequence.txt

Gln Thr Asp Lys Thr Lys Leu Lys Glu Leu Leu Gln Lys Ala Glu Thr
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Leu Lys Pro Lys Ala Gly Lys Gln Phe Thr Lys Ala Ser Gln Glu Ala
915 920 925

Leu Ala Glu Ala Ile Lys Gln Ala Lys Ala Leu Val Glu Asp Pro Asn
930 935 940

Ala Thr Gln Glu Ala Val Asp Lys Cys Leu Ser Ile Leu Ser Gln Ala
945 950 955 960

Ile Glu Ala Met Ala Glu Glu Pro Ile Ser Ser Asn Ser Thr Gly Asn
965 970 975

Asn Gly Asn His Ser Thr Val Ser Gly Thr Gly Gly Val Thr Ser Gln
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995 1000 1005

Gly Thr
1010

<210> 4
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<212> PRT
<213> Staphylococcus epidermidis

<400> 4

Glu Glu Val Asn Ser Asp Gly Gln Leu Thr Leu Gly Glu Val Lys Gln
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20 25 30

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35 40 45

P07741US01_6-19-06_Sequence.txt

Ala Ala His Trp Ala Ala Pro Asn Asn Thr Arg Lys Ile Gln Val Asp
50 55 60

Asp Gln Lys Lys Gln Ile Gln Ile Glu Leu Asn Gln Gln Ala Leu Ala
65 70 75 80

Asp Thr Leu Val Leu Thr Leu Asn Pro Thr Ala Thr Glu Asp Val Thr
85 90 95

Phe Ser Tyr Gly Gln Gln Gln Arg Ala Leu Thr Leu Lys Thr Gly Thr
100 105 110

Asp Pro Thr Glu Ser Thr Ala Ile Thr Ser Ser Pro Ala Ala Ser Ala
115 120 125

Asn Glu Gly Ser Thr Glu Glu Ala Ser Thr Asn Ser Ser Val Pro Arg
130 135 140

Ser Ser Glu Glu Thr Val Ala Ser Thr Thr Lys Ala Ile Glu Ser Lys
145 150 155 160

Thr Thr Glu Ser Thr Thr Val Lys Pro Arg Val Ala Gly Pro Thr Asp
165 170 175

Ile Ser Asp Tyr Phe Thr Gly Asp Glu Thr Thr Ile Ile Asp Asn Phe
180 185 190

Glu Asp Pro Ile Tyr Leu Asn Pro Asp Gly Thr Pro Ala Thr Pro Pro
195 200 205

Tyr Lys Glu Asp Val Thr Ile His Trp Asn Phe Asn Trp Ser Ile Pro
210 215 220

Glu Asp Val Arg Glu Gln Met Lys Ala Gly Asp Tyr Phe Glu Phe Gln
225 230 235 240

Leu Pro Gly Asn Leu Lys Pro Asn Lys Pro Gly Ser Gly Asp Leu Val
245 250 255

P07741US01_6-19-06_Sequence.txt

Asp Ala Glu Gly Asn Val Tyr Gly Thr Tyr Thr Ile Ser Glu Asp Gly
 260 265 270
 Thr Val Arg Phe Thr Phe Asn Glu Arg Ile Thr Ser Glu Ser Asp Ile
 275 280 285
 His Gly Asp Phe Ser Leu Asp Thr His Leu Asn Asp Ser Asp Gly Arg
 290 295 300
 Gly Pro Gly Asp Trp Val Ile Asp Ile Pro Thr Gln Glu Asp Leu Pro
 305 310 315 320
 Pro Val Val Ile Pro Ile Val Pro Asp Thr Glu Gln Gln Ile Asp Lys
 325 330 335
 Gln Gly His Phe Asp Arg Thr Pro Asn Pro Ser Ala Ile Thr Trp Thr
 340 345 350
 Val Asp Ile Asn Gln Ala Met Lys Asp Gln Thr Asn Pro Thr Val Thr
 355 360 365
 Glu Thr Trp Pro Thr Gly Asn Thr Phe Lys Ser Val Lys Val Tyr Glu
 370 375 380
 Leu Val Met Asn Leu Asp Gly Thr Ile Lys Glu Val Gly Arg Glu Leu
 385 390 395 400
 Ser Pro Asp Glu Tyr Thr Val Asp Lys Asn Gly Asn Val Thr Ile Lys
 405 410 415
 Gly Asp Thr Asn Lys Ala Tyr Arg Leu Glu Tyr Gln Thr Thr Ile Asp
 420 425 430
 Glu Ala Val Ile Pro Asp Gly Gly Gly Asp Val Pro Phe Lys Asn His
 435 440 445
 Ala Thr Leu Thr Ser Asp Asn Asn Pro Asn Gly Leu Asp Ala Glu Ala
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P07741US01_6-19-06_Sequence.txt

Thr Val Thr Ala Thr Tyr Gly Lys Met Leu Asp Lys Arg Asn Ile Asp
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 485 490 495
 Gly Glu Gln Thr Ile Pro Lys Asp Gln Ala Val Ile Thr Asp Thr Met
 500 505 510
 Gly Asp Asn Leu Thr Phe Glu Pro Asp Ser Leu His Leu Tyr Ser Val
 515 520 525
 Thr Phe Asp Asp Lys Gly Asn Glu Val Val Gly Ala Glu Leu Val Glu
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 Gly Lys Asp Tyr Lys Val Val Ile Asn Gly Asp Gly Ser Phe Ala Ile
 545 550 555 560
 Asp Phe Leu His Asp Val Thr Gly Ala Val Lys Ile Asp Tyr Lys Thr
 565 570 575
 Lys Val Asp Gly Ile Val Glu Gly Asp Val Ala Val Asn Asn Arg Val
 580 585 590
 Asp Val Gly Thr Gly Gln His Ser Glu Asp Asp Gly Thr Ala Ser Gln
 595 600 605
 Gln Asn Ile Ile Lys Asn Thr Gly Ala Val Asp Tyr Gln Asn Ser Thr
 610 615 620
 Ile Gly Trp Thr Leu Ala Val Asn Gln Asn Asn Tyr Leu Met Glu Asn
 625 630 635 640
 Ala Val Ile Thr Asp Thr Tyr Glu Pro Val Pro Gly Leu Thr Met Val
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 Pro Asn Ser Leu Val Val Lys Asp Thr Thr Thr Gly Ala Gln Leu Thr
 660 665 670

P07741US01_6-19-06_Sequence.txt

Leu Gly Lys Asp Phe Met Val Glu Ile Thr Arg Asn Ala Asp Gly Glu
 675 680 685
 Thr Gly Phe Lys Val Ser Phe Ile Gly Ala Tyr Ala Lys Thr Ser Asp
 690 695 700
 Ala Phe His Ile Thr Tyr Thr Thr Phe Phe Asp Val Thr Glu Leu Asp
 705 710 715 720
 Ala Asn Asn Pro Ala Leu Asp His Tyr Arg Asn Thr Ala Ala Ile Asp
 725 730 735
 Trp Thr Asp Glu Ala Gly Asn Asn His His Ser Glu Asp Ser Lys Pro
 740 745 750
 Phe Lys Pro Leu Pro Ala Phe Asp Leu Asn Ala Gln Lys Ser Gly Val
 755 760 765
 Tyr Asn Ala Val Thr Lys Glu Ile Thr Trp Thr Ile Ala Val Asn Leu
 770 775 780
 Ser Asn Asn Arg Leu Val Asp Ala Phe Leu Thr Asp Pro Ile Leu Thr
 785 790 795 800
 Asn Gln Thr Tyr Leu Ala Gly Ser Leu Lys Val Tyr Glu Gly Asn Thr
 805 810 815
 Lys Pro Asp Gly Ser Val Glu Lys Val Lys Pro Thr Gln Pro Leu Thr
 820 825 830
 Asp Ile Thr Met Glu Glu Pro Ser Glu Lys Asn Gln Asn Thr Trp Arg
 835 840 845
 Val Asp Phe Pro Asn Asp Ser Arg Thr Tyr Val Ile Glu Phe Lys Thr
 850 855 860
 Ser Val Asp Glu Lys Val Ile Glu Gly Ser Ala Ser Tyr Asp Asn Thr
 865 870 875 880

P07741US01_6-19-06_Sequence.txt

Ala Ser Tyr Thr Asn Gln Gly Ser Ser Arg Asp Val Thr Gly Lys Val
885 890 895

Ser Ile Gln His Gly Gly Glu Ser Val Lys Lys Gly Gly Glu Tyr His
900 905 910

Lys Asp Asp Pro Asp His Val Tyr Trp His Val Met Ile Asn Gly Ala
915 920 925

Gln Ser Val Leu Asp Asp Val Val Ile Thr Asp Thr Pro Ser Pro Asn
930 935 940

Gln Val Leu Asp Pro Glu Ser Leu Val Ile Tyr Gly Thr Asn Val Thr
945 950 955 960

Glu Asp Gly Thr Ile Thr Pro Asp Lys Ser Val Ile Leu Glu Glu Gly
965 970 975

Lys Asp Tyr Thr Leu Glu Val Thr Thr Asp Asn Glu Thr Gly Gln Gln
980 985 990

Lys Ile Val Val Lys Met Ala His Ile Glu Ala Pro Tyr Tyr Met Glu
995 1000 1005

Tyr Arg Ser Leu Val Thr Ser Ser Ala Ala Gly Ser Thr Asp Thr
1010 1015 1020

Val Ser Asn Gln Val Ser Ile Thr Gly Asn Gly Ser Glu Val Val
1025 1030 1035

His Gly Asp Asp Asn Gly Asp Val Val Val Asp Ile Asp His Ser
1040 1045 1050

Gly Gly His Ala Thr Gly Thr Lys Gly Lys Ile Gln Leu Lys Lys
1055 1060 1065

Thr Ala Met Asp Glu Thr Thr Ile Leu Ala Gly Ala His Phe Gln
1070 1075 1080

P07741US01_6-19-06_Sequence.txt

Ile Trp Asp Gln Ala Lys Thr Gln Val Leu Arg Glu Gly Thr Val
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<210> 5

<211> 999

<212> PRT

<213> Staphylococcus epidermidis

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Gly Glu Lys Ala Val Asp Gly Asp Glu Thr Thr Arg Trp Ser Ala Asp
35 40 45

Lys Gln Asp Glu Gln Trp Leu Ile Val Asp Leu Gly Glu Val Lys Asn
50 55 60

Ile Gly Glu Leu Val Leu Gln Leu His Ala Glu Ser Pro Val Tyr Glu
65 70 75 80

Ile Leu Val Ser Thr Asp Gly Glu Ser Tyr Gln Ser Ile Phe Lys Glu
85 90 95

Glu Asn Gly Lys Gly Gly Gln Pro Thr Lys Lys Tyr Ile Asp Gly Asn
100 105 110

Asn Val Gln Ala Arg Phe Val Lys Tyr Gln Gln Met Lys Met Trp Gln
115 120 125

His Thr Asn Lys Gln Phe Tyr Ser Ser Ser Ile Ile Ser Phe Glu Ala
130 135 140

P07741US01_6-19-06_Sequence.txt

Tyr Glu Lys Lys Arg Leu Pro Glu Ala Ile Lys Leu Leu Thr Glu Asn
 145 150 155 160
 Leu Thr Ile Ser Glu Lys Arg Lys Gln Gln Leu Ala Phe Glu Val Ser
 165 170 175
 Pro Ala Gly Val Asp Ile Thr Glu Asp Gln Ile Glu Trp Ser Ser Ser
 180 185 190
 Asp Pro Thr Ile Val Thr Val Asp Gln Thr Gly Asn Leu Thr Ala Val
 195 200 205
 Lys Ser Gly Glu Ala Lys Val Thr Val Lys Ile Lys Gly Thr Glu Ile
 210 215 220
 Ser Asp Thr Ile Pro Val Thr Val Val Ala Glu Asn Lys Gln Tyr Ala
 225 230 235 240
 Glu Met Arg Ala Lys Trp Lys Met Arg Leu Leu Gly Thr Thr Gln Tyr
 245 250 255
 Asp Asn Asp Ala Asp Val Gln Gln Tyr Arg Ala Gln Ile Ala Thr Glu
 260 265 270
 Ser Leu Ala Leu Trp Gln Thr Leu Asn Gln Ala Ala Asp Arg Glu Tyr
 275 280 285
 Leu Trp Glu Arg Lys Pro Ser Asp Thr Val Ser Ala Asp Tyr Thr Thr
 290 295 300
 Gln Phe Thr Asn Ile Lys Lys Leu Ala Leu Gly Tyr Tyr Glu Pro Ser
 305 310 315 320
 Ser Glu Leu Phe Glu Lys Pro Glu Val Tyr Asp Ala Ile Val Lys Gly
 325 330 335
 Ile Glu Phe Met Ile Asp Thr Lys Lys Tyr Asn Gly Thr Tyr Tyr Thr
 340 345 350

P07741US01_6-19-06_sequence.txt

Gly Asn Trp Trp Asp Trp Gln Ile Gly Ser Ala Gln Pro Leu Thr Asp
355 360 365

Thr Leu Ile Leu Leu His Asp Asp Leu Leu Asn Thr Asp Ala Glu Lys
370 375 380

Leu Asn Lys Phe Thr Ala Pro Leu Met Leu Tyr Ala Lys Asp Pro Asn
385 390 395 400

Ile Gln Trp Pro Ile Tyr Arg Ala Thr Gly Ala Asn Leu Thr Asp Ile
405 410 415

Ser Ile Thr Val Leu Gly Thr Gly Leu Leu Leu Glu Asp Asn Gln Arg
420 425 430

Leu Val Gln Val Gln Glu Ala Val Pro Ser Val Leu Lys Ser Val Ser
435 440 445

Ser Gly Asp Gly Leu Tyr Pro Asp Gly Ser Leu Ile Gln His Gly Tyr
450 455 460

Phe Pro Tyr Asn Gly Ser Tyr Gly Asn Glu Leu Leu Lys Gly Phe Gly
465 470 475 480

Arg Ile Gln Thr Ile Leu Gln Gly Ser Asp Trp Glu Met Asn Asp Pro
485 490 495

Asn Ile Ser Asn Leu Phe Asn Val Val Asp Lys Gly Tyr Leu Gln Leu
500 505 510

Met Val Asn Gly Lys Met Pro Ser Met Val Ser Gly Arg Ser Ile Ser
515 520 525

Arg Ala Pro Glu Thr Asn Pro Phe Thr Thr Glu Phe Glu Ser Gly Lys
530 535 540

Glu Thr Ile Ala Asn Leu Thr Leu Ile Ala Lys Phe Ala Pro Glu Asn
545 550 555 560

P07741US01_6-19-06_Sequence.txt

Leu Arg Asn Asp Ile Tyr Thr Ser Ile Gln Thr Trp Leu Gln Gln Ser
565 570 575

Gly Ser Tyr Tyr His Phe Phe Lys Lys Pro Arg Asp Phe Glu Ala Leu
580 585 590

Ile Asp Leu Lys Asn Val Val Asn Ser Ala Ser Pro Ala Gln Ala Thr
595 600 605

Pro Met Gln Ser Leu Asn Val Tyr Gly Ser Met Asp Arg Val Leu Gln
610 615 620

Lys Asn Asn Glu Tyr Ala Val Gly Ile Ser Met Tyr Ser Gln Arg Val
625 630 635 640

Gly Asn Tyr Glu Phe Gly Asn Thr Glu Asn Lys Lys Gly Trp His Thr
645 650 655

Ala Asp Gly Met Leu Tyr Leu Tyr Asn Gln Asp Phe Ala Gln Phe Asp
660 665 670

Glu Gly Tyr Trp Ala Thr Ile Asp Pro Tyr Arg Leu Pro Gly Thr Thr
675 680 685

Val Asp Thr Arg Glu Leu Ala Asn Gly Ala Tyr Thr Gly Lys Arg Ser
690 695 700

Pro Gln Ser Trp Val Gly Gly Ser Asn Asn Gly Gln Val Ala Ser Ile
705 710 715 720

Gly Met Phe Leu Asp Lys Ser Asn Glu Gly Met Asn Leu Val Ala Lys
725 730 735

Lys Ser Trp Phe Leu Leu Asp Gly Gln Ile Ile Asn Leu Gly Ser Gly
740 745 750

Ile Thr Gly Thr Thr Asp Ala Ser Ile Glu Thr Ile Leu Asp Asn Arg
755 760 765

P07741US01_6-19-06_Sequence.txt

Met Ile His Pro Gln Glu Val Lys Leu Asn Gln Gly Ser Asp Lys Asp
770 775 780

Asn Ser Trp Ile Ser Leu Ser Ala Ala Asn Pro Leu Asn Asn Ile Gly
785 790 795 800

Tyr Val Phe Pro Asn Ser Met Asn Thr Leu Asp Val Gln Ile Glu Glu
805 810 815

Arg Ser Gly Arg Tyr Gly Asp Ile Asn Glu Tyr Phe Val Asn Asp Lys
820 825 830

Thr Tyr Thr Asn Thr Phe Ala Lys Ile Ser Lys Asn Tyr Gly Lys Thr
835 840 845

Val Glu Asn Gly Thr Tyr Glu Tyr Leu Thr Val Val Gly Lys Thr Asn
850 855 860

Glu Glu Ile Ala Ala Leu Ser Lys Asn Lys Gly Tyr Thr Val Leu Glu
865 870 875 880

Asn Thr Ala Asn Leu Gln Ala Ile Glu Ala Gly Asn Tyr Val Met Met
885 890 895

Asn Thr Trp Asn Asn Asp Gln Glu Ile Ala Gly Leu Tyr Ala Tyr Asp
900 905 910

Pro Met Ser Val Ile Ser Glu Lys Ile Asp Asn Gly Val Tyr Arg Leu
915 920 925

Thr Leu Ala Asn Pro Leu Gln Asn Asn Ala Ser Val Ser Ile Glu Phe
930 935 940

Asp Lys Gly Ile Leu Glu Val Val Ala Ala Asp Pro Glu Ile Ser Val
945 950 955 960

Asp Gln Asn Ile Ile Thr Leu Asn Ser Ala Gly Leu Asn Gly Ser Ser
965 970 975

P07741US01_6-19-06_Sequence.txt

Arg Ser Ile Ile Val Lys Thr Thr Pro Glu Val Thr Lys Glu Ala Leu
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Glu Lys Leu Ile Gln Glu Gln
995

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<212> PRT
<213> Staphylococcus epidermidis

<400> 6

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Thr Val Thr Tyr Glu Val Thr Asn Thr Arg Asp Val Pro Ile Lys Asp
35 40 45

Leu Ile Leu Lys Gln Lys Asn Thr Asn Asp Ser Pro Ile Lys Phe Val
50 55 60

Leu Asp Thr Leu Ser Glu Glu Arg Gly Pro Thr Ser Leu Glu Glu Gln
65 70 75 80

Ala Lys Val Glu Thr Asn Glu Lys Asp Gln Thr Thr Asp Ile Lys Leu
85 90 95

Leu Asn Leu Gln Pro Asn Ser Thr Arg Lys Ile Thr Ile Asn Gly Gln
100 105 110

Ile Thr Thr Lys Ala Ser Asn Lys Leu Leu Val Ser Val Leu Ile Glu
115 120 125

Asp Asn Glu Lys Gly Thr Leu Val Ile Asp Leu Pro Ser Lys Asp Ile
130 135 140

Leu Ala Asp Lys Glu Ser Val Ser Lys Glu Lys Gln Glu Thr Ser Glu
Page 21

145 150 155 160
 Thr Lys Val Glu Asn Gln Ala Asn Glu Thr Ala Ser Ser Thr Asn Glu
 165 170 175
 Met Thr Ala Thr Thr Ser Asn Glu Thr Lys Pro Glu Ala Gly Lys Ala
 180 185 190
 Ile Glu Ser Ile Gln Glu Thr Ala Leu Thr Gln Ala Thr Glu Ser Pro
 195 200 205
 Glu Gln Pro Pro Leu Lys Ala Gln Pro Thr Gly Pro Leu Val Pro Pro
 210 215 220
 Thr Pro Gly Arg Gly Phe Asn Thr Pro Ile Tyr Gln Ser Val His Lys
 225 230 235 240
 Gly Glu Leu Phe Ser Thr Gly Asn Thr Asn Leu Lys Ile Ala Asn Glu
 245 250 255
 Asn Thr Ala Ala Ala Gln Thr Phe Leu Asn Thr Arg Gly Ala Ser Ser
 260 265 270
 Gly Tyr Ala Ile Asn Asn Phe Pro Leu Glu Phe Ala Asp Val Asp Asn
 275 280 285
 Asp Pro Asn Thr Tyr Asn Ser Ser Arg Ala Tyr Ile Asp Leu Asn Gly
 290 295 300
 Ala Lys Glu Ile Ala Trp Ala Gly Leu Phe Trp Ser Ala Ser Arg Tyr
 305 310 315 320
 Lys Gly Pro Ala Tyr Gly Thr Asn Leu Ser Asp Glu Glu Ile Ser Ala
 325 330 335
 Pro Val Gln Phe Thr Thr Pro Asn Gly Thr Val Gln Arg Val Ser Pro
 340 345 350
 Gln Arg Tyr His Arg Ile Asp Gln Asp Ala Thr Asn Pro Gly Gln Arg

P07741US01_6-19-06_sequence.txt

355

360

365

Phe Gly Tyr Asn Asn Thr Gly Phe Ser Asn Tyr Ala Asp Val Thr Ser
370 375 380

Ile Leu Gln Gly Asp Lys Ser Ala Thr Gly Ser Tyr Thr Leu Ala Asp
385 390 395 400

Ile Pro Met Thr Ser Ser Leu Asn Gly Gln Tyr Gln Tyr Tyr Asn Phe
405 410 415

Ser Gly Trp Ser Leu Phe Val Val Thr Lys Asp Gln Ala Ser Lys Ser
420 425 430

Arg Ala Phe Ser Ile Tyr Tyr Gly Ala Arg Gly Asn Ala Ala Gly Thr
435 440 445

Asn Asn Glu Phe Thr Met Ser Asn Phe Leu Thr Ala Lys Gln Gly Asn
450 455 460

Leu Asp Pro Ile Val Thr Trp Phe Thr Val Gln Gly Asp Lys Tyr Trp
465 470 475 480

Thr Gly Asp Asn Ala Gln Ile Lys Asn Ser Ala Gly Thr Trp Val Asn
485 490 495

Ile Ser Asn Thr Leu Asn Pro Val Asn Asn Ala Met Asn Ala Thr Val
500 505 510

Thr Asp Asn Asp Glu His Met Val Asp Lys Tyr Pro Gly Lys Phe Ala
515 520 525

Pro Asp His Pro Asn Phe Leu Asp Ile Asp Ile Asp Arg Met Ala Ile
530 535 540

Pro Glu Gly Val Leu Asn Ala Gly Gln Asn Gln Ile Asn Phe Arg Thr
545 550 555 560

Thr Ser Ser Gly Asp Asp Tyr Ser Thr Asn Ala Ile Gly Phe Ala Val
Page 23

Asn Ala Glu Thr Pro Glu Phe Glu Ile Lys Lys Glu Ile Val Glu Pro
580 585 590

Lys Glu Thr Tyr Lys Val Gly Glu Thr Ile Thr Tyr Arg Val Ser Leu
595 600 605

Lys Asn Thr Lys Ala Asp Ser Glu Ala Ile Asn Ser Val Ser Lys Asp
610 615 620

Ala Leu Asp Gly Arg Leu Asn Tyr Leu Pro Gly Ser Leu Lys Ile Ile
625 630 635 640

Ser Gly Pro Asn Ser Gly Glu Lys Thr Asp Ala Ser Gly Asp Asp Gln
645 650 655

Ala Glu Tyr Asp Glu Thr Asn Lys Gln Ile Ile Val Arg Val Gly Asn
660 665 670

Gly Ala Thr Ala Thr Gln Gly Gly Ser Tyr Lys Ala Asp Thr Ala Glu
675 680 685

Thr Ile Tyr Glu Phe Lys Ala Arg Ile Asn Glu Arg Ala Lys Ala Asn
690 695 700

Glu Leu Val Pro Asn Ser Ala Thr Val Glu Ala Val Asp Ile Leu Thr
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725 730 735

Asp Glu Gln Val Thr
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<210> 7
<211> 570
<212> PRT
<213> Staphylococcus epidermidis

<400> 7

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 35 40 45
 Thr Ile Asn Gln Tyr Thr Asp Ile Tyr Leu Arg Ile Glu Phe Asn Leu
 50 55 60
 Pro Asp Asn Thr Val Asn Ser Gly Asp Thr Ser Val Ile Thr Leu Pro
 65 70 75 80
 Glu Glu Leu Arg Leu Glu Lys Asn Met Thr Phe Asn Val Val Asp Asp
 85 90 95
 Thr Gly Thr Val Val Ala Ile Ala Gln Thr Asp Val Ala Asn Lys Thr
 100 105 110
 Val Thr Leu Thr Tyr Thr Asp Tyr Val Glu Asn His Ala Asn Ile Ser
 115 120 125
 Gly Ser Leu Tyr Phe Thr Ser Leu Ile Asp Phe Glu Asn Val Glu Asn
 130 135 140
 Glu Ser Lys Ile Pro Ile Tyr Val Thr Val Glu Gly Glu Lys Ile Phe
 145 150 155 160
 Ala Gly Asp Leu Asp Tyr Gln Gly Glu Gly Asp Asp Val Asn Glu Lys
 165 170 175
 Phe Ser Lys Tyr Ser Trp Phe Ile Glu Asp Asp Pro Thr Glu Ile Tyr
 180 185 190
 Asn Val Leu Arg Ile Asn Pro Thr Gly Gln Thr Tyr Thr Asp Leu Glu
 195 200 205

P07741US01_6-19-06_Sequence.txt

Val Glu Asp Val Leu Lys Thr Glu Ser Leu Ser Tyr Met Lys Asp Thr
 210 215 220
 Met Lys Ile Glu Arg Gly Gln Trp Thr Leu Asp Gly Asn Ala Ile Trp
 225 230 235 240
 Gln Phe Thr Pro Glu Glu Asp Ile Thr Asp Gln Leu Ala Val Gln Tyr
 245 250 255
 Gly Pro Asp Asp Arg Asn Phe Ser Val His Phe Gly Asn Ile Gly Thr
 260 265 270
 Asn Glu Tyr Arg Ile Thr Tyr Lys Thr Lys Ile Asp His Leu Pro Glu
 275 280 285
 Lys Gly Glu Thr Phe Thr Asn Tyr Ala Lys Leu Thr Glu Asn Gln Thr
 290 295 300
 Val Val Glu Glu Val Glu Val Ser Arg Val Ser Gln Thr Gly Gly Gly
 305 310 315 320
 Glu Ala Asn Gly Glu Gln Tyr Val Val Glu Ile His Lys Glu Asp Glu
 325 330 335
 Ala Gly Gln Arg Leu Ala Gly Ala Glu Phe Glu Leu Ile Arg Asn Ser
 340 345 350
 Thr Asn Gln Thr Val Ala Lys Ile Thr Thr Asp Gln Asn Gly Thr Ala
 355 360 365
 Ile Val Lys Gly Leu Leu Lys Asp Asn Tyr Thr Leu Val Glu Thr Lys
 370 375 380
 Ala Pro Thr Gly Tyr Gln Leu Ser Gln Asn Lys Ile Pro Ile Thr Pro
 385 390 395 400
 Glu Asp Phe Gly Lys Asn Leu Val Ala Leu Lys Thr Val Val Asn His
 405 410 415

P07741US01_6-19-06_Sequence.txt

Lys Ile Ser Tyr Gln Pro Val Ala Ala Ser Phe Leu Ala Gly Lys Val
420 425 430

Leu Leu Gly Lys Pro Leu Lys Asp Ala Glu Phe Gln Phe Glu Leu Leu
435 440 445

Asp Glu Lys Gly Thr Val Leu Glu Thr Val Ser Asn Asp Thr Leu Gly
450 455 460

Lys Ile Gln Phe Ser Pro Leu Thr Phe Glu Thr Pro Gly Asn Tyr Gln
465 470 475 480

Tyr Thr Ile Arg Glu Val Asn Thr Gln Gln Thr Gly Val Ser Tyr Asp
485 490 495

Thr His Asn Leu Gln Val Gln Val Thr Val Glu Ala Leu Leu Gly Asn
500 505 510

Leu Val Ala Thr Thr Gln Tyr Asp Gly Gly Gln Val Phe Thr Asn His
515 520 525

Tyr Thr Pro Glu Lys Pro Ile Glu Ser Thr Thr Pro Pro Thr Ser Gly
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545 550 555 560

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<210> 8
<211> 3309
<212> DNA
<213> Staphylococcus epidermidis

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acagagcagc cattacaacg agaaattcaa ttgaaaaatg cacagttcat ggatactgct
Page 27

120

gtaattgaaa aagacggata ttcttaccaa gtgactaatg gtacgcttta tctgactttg
180

gacgcacaag taaaaaagcc ggtacagctt tcgttagctg ttgagcaaag ttcgcttcaa
240

acagctcagc cacctaagtt attgtatgaa aacaacgaat atgatgtttc agttacttct
300

gaaaaaataa cagtagagga ttctgctaaa gaatcaactg aaccagaaaa aataactgta
360

ccagaaaata cgaaagaaac taacaaaaat gattcggctc cagaaaaaac agaacagccg
420

accgcaacag aagaggtaac caatccattt gcagaagcaa gaatggcgcc agctactttg
480

agagcgaatc tggcactgcc ttttaattgca ccacaataca cgacggataa ttctgggact
540

tatccgacag ctaattggca gcccacaggc aatcaaaatg tgttaaacca tcaagggaat
600

aaagacggta gtgcacaatg ggacggccaa acgagttgga atggggaccc tactaatcgc
660

acaaattctt atattgagta tggcgggtaca ggagaccaag ccgattatgc catccgaaaa
720

tatgctagag aaacaacaac accagggctt tttgatgtat atcttaatgt gcgtgggaat
780

gttcagaaaag aaatcacgcc attggatttg gtcttagtcg ttgactgggc cggtagtatg
840

aatgaaaaca atcggattgg tgaagttcaa aaaggagtga accgttttgt tgatacattg
900

gcagatagcg gtattaccaa taacatcaac atgggctatg ttggctactc aagtgcgggt
960

tataataaca acgccattca aatggggccg tttgatacag tcaaaaatcc aattaaaaat
1020

attacgccaa gtagcactag aggaggaact ttcactcaaa aagcattaag agatgctggg
1080

gatatgttag caacgccaaa tggacataag aaagtcattg tacttttaac ggatggcgctc
1140

P07741US01_6-19-06_Sequence.txt

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acacaattta cgaatcgaca agatcaacca ggtagcactt cttatatctc tggtagctat
1260

aatgcgccag atcaaaacaa tatcaataaa cggattaaca gtacgtttat cgccacgata
1320

ggtgaggcaa tgggtcttaaa acaacgtggg attgaaatac atggattggg cattcaattg
1380

caaagcgatc cacgagctaa tttatctaaa caacaagttg aagataaaat gcgtgagatg
1440

gtgtcagccg atgaaaatgg agacctttat tatgaatccg cggattatgc accagacatt
1500

tctgattatt tagcgaaaaa agccgttcag atttcaggaa cggttgtaaa cggaagaagta
1560

gttgatccaa ttgctgaacc ttttaaatac gagccaaata cattatcaat gaaaagtgtg
1620

ggtcctgttc aggttcaaac attaccagaa gtgtcgctaa caggcgctac aattaatagt
1680

aatgagattt atttgggtaa agggcaagaa attcaaattc attatcaagt acgtattcaa
1740

acagagtcag aaaacttcaa acctgatttt tggtatcaaa tgaatggtcg gacaacgttt
1800

cagccattag ccacggcccc tgaaaaagtt gattttgggg ttccttcggg aaaagcacct
1860

ggcgtgaagt taaacgtgaa aaaaatctgg gaagagtatg atcaagaccc gacaagtcgg
1920

ccagataatg tgatttatga aattagtaga aagcaagtaa ctgacacagc caactggcaa
1980

actgggtata ttaaattatc aaaaccagaa aatgatacca gcaatagttg ggagcgcaaa
2040

aatgtaaccc aactttccaa aaccgcggat gaaagctatc aagaagttct tgggcttccc
2100

caatacaaca atcaaggaca agctttcaat tatcaaacaa cccgtgaatt agcagttcct
2160

P07741US01_6-19-06_Sequence.txt

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ttagatttaa aagtaatcaa aaattcttcc tcagggtgaga aaaacttagt gggagccgct
2280

tttgaattga gtggtaaaaa tgttcaaaca acattagtgg acaataaaga tggtagctat
2340

tccttgccaa aagatgtgcg cctacaaaaa ggggaacgct atacattaac tgaagtaaaa
2400

gcacctgcag gacatgagtt aggcaagaaa acgacttggc aaattgaggt gagtgagcaa
2460

ggcaaagtaa gcatcgatgg acaagaagtg accaccacaa atcaagttat tccattggaa
2520

attgaaaata aattttcttc tttgccaatc agaattagaa aatacaccat gcaaaatggc
2580

aaacaagtga acttagcaga ggcgactttt gcgttgcaaa gaaaaaatgc tcaaggaagt
2640

taccaaactg tggcaactca aaaaacagat actacaggat tgagctatatt taaaattagt
2700

gaacctggtg agtatcgaat ggtggaacaa tcaggaccat taggctacga cactcttgct
2760

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2820

gaagaaaatg cgccagaatg gacactgaca catcaaaata atttgaaacc ttttgactta
2880

acagttaata aaaaagccga taatcagacg ccacttaaag gagcgaaatt ccgtttaaca
2940

ggaccagata cggatattga attaccaaaa gatggcaaag aaacggatac ttttgttttt
3000

gaaaacttaa aaccagggaa atatgttcta acagaaacct ttacgccaga aggatatcag
3060

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3120

gaaaaagtag cagatgtttt aatttctgga gagaagaata atcaaattac tttagacggt
3180

acgaaccaag caaaggttcc tttacctgaa actggtggca taggacgctt gtggtttttac
Page 30

3240

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3300

gggagtgtg
3309

<210> 9
<211> 1103
<212> PRT
<213> Staphylococcus epidermidis

<400> 9

Met Ile Thr Asp Glu Asn Asp Lys Thr Asn Ile Asn Ile Glu Leu Asn
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Leu Leu Asn Gln Thr Glu Gln Pro Leu Gln Arg Glu Ile Gln Leu Lys
20 25 30

Asn Ala Gln Phe Met Asp Thr Ala Val Ile Glu Lys Asp Gly Tyr Ser
35 40 45

Tyr Gln Val Thr Asn Gly Thr Leu Tyr Leu Thr Leu Asp Ala Gln Val
50 55 60

Lys Lys Pro Val Gln Leu Ser Leu Ala Val Glu Gln Ser Ser Leu Gln
65 70 75 80

Thr Ala Gln Pro Pro Lys Leu Leu Tyr Glu Asn Asn Glu Tyr Asp Val
85 90 95

Ser Val Thr Ser Glu Lys Ile Thr Val Glu Asp Ser Ala Lys Glu Ser
100 105 110

Thr Glu Pro Glu Lys Ile Thr Val Pro Glu Asn Thr Lys Glu Thr Asn
115 120 125

Lys Asn Asp Ser Ala Pro Glu Lys Thr Glu Gln Pro Thr Ala Thr Glu
130 135 140

P07741US01_6-19-06_Sequence.txt

Glu Val Thr Asn Pro Phe Ala Glu Ala Arg Met Ala Pro Ala Thr Leu
 145 150 155 160
 Arg Ala Asn Leu Ala Leu Pro Leu Ile Ala Pro Gln Tyr Thr Thr Asp
 165 170 175
 Asn Ser Gly Thr Tyr Pro Thr Ala Asn Trp Gln Pro Thr Gly Asn Gln
 180 185 190
 Asn Val Leu Asn His Gln Gly Asn Lys Asp Gly Ser Ala Gln Trp Asp
 195 200 205
 Gly Gln Thr Ser Trp Asn Gly Asp Pro Thr Asn Arg Thr Asn Ser Tyr
 210 215 220
 Ile Glu Tyr Gly Gly Thr Gly Asp Gln Ala Asp Tyr Ala Ile Arg Lys
 225 230 235 240
 Tyr Ala Arg Glu Thr Thr Thr Pro Gly Leu Phe Asp Val Tyr Leu Asn
 245 250 255
 Val Arg Gly Asn Val Gln Lys Glu Ile Thr Pro Leu Asp Leu Val Leu
 260 265 270
 Val Val Asp Trp Ser Gly Ser Met Asn Glu Asn Asn Arg Ile Gly Glu
 275 280 285
 Val Gln Lys Gly Val Asn Arg Phe Val Asp Thr Leu Ala Asp Ser Gly
 290 295 300
 Ile Thr Asn Asn Ile Asn Met Gly Tyr Val Gly Tyr Ser Ser Asp Gly
 305 310 315 320
 Tyr Asn Asn Asn Ala Ile Gln Met Gly Pro Phe Asp Thr Val Lys Asn
 325 330 335
 Pro Ile Lys Asn Ile Thr Pro Ser Ser Thr Arg Gly Gly Thr Phe Thr
 340 345 350

P07741US01_6-19-06_Sequence.txt

Gln Lys Ala Leu Arg Asp Ala Gly Asp Met Leu Ala Thr Pro Asn Gly
355 360 365

His Lys Lys Val Ile Val Leu Leu Thr Asp Gly Val Pro Thr Phe Ser
370 375 380

Tyr Lys Val Ser Arg Val Gln Thr Glu Ala Asp Gly Arg Phe Tyr Gly
385 390 395 400

Thr Gln Phe Thr Asn Arg Gln Asp Gln Pro Gly Ser Thr Ser Tyr Ile
405 410 415

Ser Gly Ser Tyr Asn Ala Pro Asp Gln Asn Asn Ile Asn Lys Arg Ile
420 425 430

Asn Ser Thr Phe Ile Ala Thr Ile Gly Glu Ala Met Val Leu Lys Gln
435 440 445

Arg Gly Ile Glu Ile His Gly Leu Gly Ile Gln Leu Gln Ser Asp Pro
450 455 460

Arg Ala Asn Leu Ser Lys Gln Gln Val Glu Asp Lys Met Arg Glu Met
465 470 475 480

Val Ser Ala Asp Glu Asn Gly Asp Leu Tyr Tyr Glu Ser Ala Asp Tyr
485 490 495

Ala Pro Asp Ile Ser Asp Tyr Leu Ala Lys Lys Ala Val Gln Ile Ser
500 505 510

Gly Thr Val Val Asn Gly Lys Val Val Asp Pro Ile Ala Glu Pro Phe
515 520 525

Lys Tyr Glu Pro Asn Thr Leu Ser Met Lys Ser Val Gly Pro Val Gln
530 535 540

Val Gln Thr Leu Pro Glu Val Ser Leu Thr Gly Ala Thr Ile Asn Ser
545 550 555 560

P07741US01_6-19-06_Sequence.txt

Asn Glu Ile Tyr Leu Gly Lys Gly Gln Glu Ile Gln Ile His Tyr Gln
565 570 575

Val Arg Ile Gln Thr Glu Ser Glu Asn Phe Lys Pro Asp Phe Trp Tyr
580 585 590

Gln Met Asn Gly Arg Thr Thr Phe Gln Pro Leu Ala Thr Ala Pro Glu
595 600 605

Lys Val Asp Phe Gly Val Pro Ser Gly Lys Ala Pro Gly Val Lys Leu
610 615 620

Asn Val Lys Lys Ile Trp Glu Glu Tyr Asp Gln Asp Pro Thr Ser Arg
625 630 635 640

Pro Asp Asn Val Ile Tyr Glu Ile Ser Arg Lys Gln Val Thr Asp Thr
645 650 655

Ala Asn Trp Gln Thr Gly Tyr Ile Lys Leu Ser Lys Pro Glu Asn Asp
660 665 670

Thr Ser Asn Ser Trp Glu Arg Lys Asn Val Thr Gln Leu Ser Lys Thr
675 680 685

Ala Asp Glu Ser Tyr Gln Glu Val Leu Gly Leu Pro Gln Tyr Asn Asn
690 695 700

Gln Gly Gln Ala Phe Asn Tyr Gln Thr Thr Arg Glu Leu Ala Val Pro
705 710 715 720

Gly Tyr Ser Gln Glu Lys Ile Asp Asp Thr Thr Trp Lys Asn Thr Lys
725 730 735

Gln Phe Lys Pro Leu Asp Leu Lys Val Ile Lys Asn Ser Ser Ser Gly
740 745 750

Glu Lys Asn Leu Val Gly Ala Val Phe Glu Leu Ser Gly Lys Asn Val
755 760 765

P07741US01_6-19-06_Sequence.txt

Gln Thr Thr Leu Val Asp Asn Lys Asp Gly Ser Tyr Ser Leu Pro Lys
770 775 780

Asp Val Arg Leu Gln Lys Gly Glu Arg Tyr Thr Leu Thr Glu Val Lys
785 790 795 800

Ala Pro Ala Gly His Glu Leu Gly Lys Lys Thr Thr Trp Gln Ile Glu
805 810 815

Val Ser Glu Gln Gly Lys Val Ser Ile Asp Gly Gln Glu Val Thr Thr
820 825 830

Thr Asn Gln Val Ile Pro Leu Glu Ile Glu Asn Lys Phe Ser Ser Leu
835 840 845

Pro Ile Arg Ile Arg Lys Tyr Thr Met Gln Asn Gly Lys Gln Val Asn
850 855 860

Leu Ala Glu Ala Thr Phe Ala Leu Gln Arg Lys Asn Ala Gln Gly Ser
865 870 875 880

Tyr Gln Thr Val Ala Thr Gln Lys Thr Asp Thr Thr Gly Leu Ser Tyr
885 890 895

Phe Lys Ile Ser Glu Pro Gly Glu Tyr Arg Met Val Glu Gln Ser Gly
900 905 910

Pro Leu Gly Tyr Asp Thr Leu Ala Gly Asn Tyr Glu Phe Thr Val Asp
915 920 925

Lys Tyr Gly Lys Ile His Tyr Ala Gly Lys Asn Ile Glu Glu Asn Ala
930 935 940

Pro Glu Trp Thr Leu Thr His Gln Asn Asn Leu Lys Pro Phe Asp Leu
945 950 955 960

Thr Val Asn Lys Lys Ala Asp Asn Gln Thr Pro Leu Lys Gly Ala Lys
965 970 975

P07741US01_6-19-06_Sequence.txt

Phe Arg Leu Thr Gly Pro Asp Thr Asp Ile Glu Leu Pro Lys Asp Gly
980 985 990

Lys Glu Thr Asp Thr Phe Val Phe Glu Asn Leu Lys Pro Gly Lys Tyr
995 1000 1005

Val Leu Thr Glu Thr Phe Thr Pro Glu Gly Tyr Gln Gly Leu Lys
1010 1015 1020

Glu Pro Ile Glu Leu Ile Ile Arg Glu Asp Gly Ser Val Thr Ile
1025 1030 1035

Asp Gly Glu Lys Val Ala Asp Val Leu Ile Ser Gly Glu Lys Asn
1040 1045 1050

Asn Gln Ile Thr Leu Asp Val Thr Asn Gln Ala Lys Val Pro Leu
1055 1060 1065

Pro Glu Thr Gly Gly Ile Gly Arg Leu Trp Phe Tyr Leu Ile Ala
1070 1075 1080

Ile Ser Thr Phe Val Ile Ala Gly Val Tyr Leu Phe Ile Arg Arg
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Pro Glu Gly Ser Val
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<210> 10
<211> 1428
<212> DNA
<213> Staphylococcus epidermidis

<400> 10
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120

ttccctgatg gtcaattacc agaacagcag caaaacacag gggaagaggg aacgctgctt
180

caaaattatc ggggcttaaa tgacgtcact tatcaagtct atgatgtgac ggatccggtt
Page 36

P07741US01_6-19-06_Sequence.txt

240

tatcagcttc gttctgaagg aaaaacggtc caagaggcac agcgtcaatt agcagaaacc
300

ggtgcaacaa atagaaaacc gatcgcagaa gataaaacac agacaataaa tggagaagat
360

ggagtggttt ctttttcatt agctagcaaa gattcgcagc aacgagataa agcctattta
420

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480

ttgcctgttc aagatccaca agggcaatcg ttaacgcata ttcatttata tccaaaaaat
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gaagaaaatg cctatgactt accaccactt gaaaaaacgg tactcgataa gcaacaaggc
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660

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720

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780

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900

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1080

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1140

gttaaaggct taaaagatgg ccagtacttc ttggaagaaa tctctgcacc aaaaggttat
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cttctgaatc aaacagaaat tccttttacg gtgggaaaaa attcttatgc aacgaacgga
1260

P07741US01_6-19-06_Sequence.txt

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1380

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1428

<210> 11

<211> 476

<212> PRT

<213> Staphylococcus epidermidis

<400> 11

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Gln Val Thr Leu His Lys Leu Leu Phe Pro Asp Gly Gln Leu Pro Glu
35 40 45

Gln Gln Gln Asn Thr Gly Glu Glu Gly Thr Leu Leu Gln Asn Tyr Arg
50 55 60

Gly Leu Asn Asp Val Thr Tyr Gln Val Tyr Asp Val Thr Asp Pro Phe
65 70 75 80

Tyr Gln Leu Arg Ser Glu Gly Lys Thr Val Gln Glu Ala Gln Arg Gln
85 90 95

Leu Ala Glu Thr Gly Ala Thr Asn Arg Lys Pro Ile Ala Glu Asp Lys
100 105 110

Thr Gln Thr Ile Asn Gly Glu Asp Gly Val Val Ser Phe Ser Leu Ala
115 120 125

Ser Lys Asp Ser Gln Gln Arg Asp Lys Ala Tyr Leu Phe Val Glu Ala
130 135 140

P07741US01_6-19-06_Sequence.txt

Glu	Ala	Pro	Glu	Val	Val	Lys	Glu	Lys	Ala	Ser	Asn	Leu	Val	Val	Ile
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Leu	Pro	Val	Gln	Asp	Pro	Gln	Gly	Gln	Ser	Leu	Thr	His	Ile	His	Leu
				165					170					175	
Tyr	Pro	Lys	Asn	Glu	Glu	Asn	Ala	Tyr	Asp	Leu	Pro	Pro	Leu	Glu	Lys
			180					185					190		
Thr	Val	Leu	Asp	Lys	Gln	Gln	Gly	Phe	Asn	Gln	Gly	Glu	His	Ile	Asn
		195					200					205			
Tyr	Gln	Leu	Thr	Thr	Gln	Ile	Pro	Ala	Asn	Ile	Leu	Gly	Tyr	Gln	Glu
	210					215					220				
Phe	Arg	Leu	Ser	Asp	Lys	Ala	Asp	Thr	Thr	Leu	Thr	Leu	Leu	Pro	Glu
225					230					235					240
Ser	Ile	Glu	Val	Lys	Val	Ala	Gly	Lys	Thr	Val	Thr	Thr	Gly	Tyr	Thr
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Leu	Thr	Thr	Gln	Lys	His	Gly	Phe	Thr	Leu	Asp	Phe	Ser	Ile	Lys	Asp
			260					265					270		
Leu	Gln	Asn	Phe	Ala	Asn	Gln	Thr	Met	Thr	Val	Ser	Tyr	Gln	Met	Arg
		275					280					285			
Leu	Glu	Lys	Thr	Ala	Glu	Pro	Asp	Thr	Ala	Ile	Asn	Asn	Glu	Gly	Gln
	290					295					300				
Leu	Val	Thr	Asp	Lys	His	Thr	Leu	Thr	Lys	Arg	Ala	Thr	Val	Arg	Thr
305					310					315					320
Gly	Gly	Lys	Ser	Phe	Val	Lys	Val	Asp	Ser	Glu	Asn	Ala	Lys	Ile	Thr
				325					330					335	
Leu	Pro	Glu	Ala	Val	Phe	Ile	Val	Lys	Asn	Gln	Ala	Gly	Glu	Tyr	Leu
			340					345					350		

P07741US01_6-19-06_Sequence.txt

Asn Glu Thr Ala Asn Gly Tyr Arg Trp Gln Lys Glu Lys Ala Leu Ala
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Lys Lys Phe Thr Ser Asn Gln Ala Gly Glu Phe Ser Val Lys Gly Leu
370 375 380

Lys Asp Gly Gln Tyr Phe Leu Glu Glu Ile Ser Ala Pro Lys Gly Tyr
385 390 395 400

Leu Leu Asn Gln Thr Glu Ile Pro Phe Thr Val Gly Lys Asn Ser Tyr
405 410 415

Ala Thr Asn Gly Gln Arg Thr Ala Pro Leu His Val Ile Asn Lys Lys
420 425 430

Val Lys Glu Ser Gly Phe Leu Pro Lys Thr Asn Glu Glu Arg Ser Ile
435 440 445

Trp Leu Thr Ile Ala Gly Leu Leu Ile Ile Gly Met Val Val Ile Trp
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Leu Phe Tyr Gln Lys Gln Lys Arg Gly Glu Arg Lys
465 470 475

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120

ctcgtgattc acaaaaagaa aatgacggat ttaccagatc cgcttattca aaatagcggg
180

aaagaaatga gcgagtttga taaatatcaa ggactggcag atgtgacgtt tagtatttat
240

P07741US01_6-19-06_Sequence.txt

aacgtgacga acgaatttta cgagcaacga gcggcaggcg caagcgttga tgcagctaaa
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360

gggaatgtca ctgttcagtt acctaaaaaa caaaatggta aagatgcagt gtataccatt
420

aaagaagaac caaaagaggg tgtagttgct gctacgaata tgggtggtggc gttcccagtt
480

tacgaaatga tcaagcaaac agatgggttcc tataaatatg gaacagaaga attagcggtt
540

gttcatatatt atcctaaaaa tgtggtagcc aatgatggta gtttacatgt gaaaaaagta
600

ggaactgctg aaaatgaagg attaaatggc gcagaatttg ttatttctaa aagcgaaggc
660

tcaccaggca cagtaaaata tatccaagga gtcaaagatg gattatatac atggacaacg
720

gataaagaac aagcaaaacg ctttattact gggaaaagtt atgaaattgg cgaaaatgat
780

ttcacagaag cagagaatgg aacgggagaa ttaacagtta aaaatcttga ggttggttcg
840

tatatatttag aagaagtaaa agctccaaat aatgcagaat taattgaaaa tcaaacaaaa
900

acaccattta caattgaagc aaacaatcaa acacctgttg aaaaaacagt caaaaatgat
960

acctctaaag ttgataaaac aacaccaagc ttagatggta aagatgtggc aattggcgaa
1020

aaaattaaat atcaaatttc tgtaaattatt ccattgggga ttgcagacaa agaaggcgac
1080

gctaataaat acgtcaaatt caatttagtt gataaacatg atgcagcctt aacttttgat
1140

aacgtgactt ctggagagta tgcttatgcg ttatatgatg gggatacagt gattgctcct
1200

gaaaattatc aagtgactga acaagcaaatt ggcttcactg tcgccgttaa tccagcgtat
1260

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1320

aaagcagatc ctacgaaagg ctttaaaaat gaggcgaatg ttgataacgg tcataccgac
1380

gaccaaacac caccaactgt tgaagttgtg acaggtggga aacgtttcat taaagtcgat
1440

ggcgatgtga cagcgacaca agccttggcg ggagcttcct ttgtcgtccg tgatcaaaac
1500

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1560

acaaaagctg aagcaactac ttttacaaca acggctgatg gattagttga tatcacaggg
1620

cttaaatacg gtacctatta tttagaagaa actgtagctc ctgatgatta tgtcttgta
1680

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1740

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<211> 627

<212> PRT

<213> Staphylococcus epidermidis

<400> 13

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Ile Leu Pro Leu Phe Thr Ser Val Leu Gly Thr Thr Thr Ala Phe Ala
20 25 30

Glu Glu Asn Gly Glu Ser Ala Gln Leu Val Ile His Lys Lys Lys Met
35 40 45

P07741US01_6-19-06_Sequence.txt

Thr Asp Leu Pro Asp Pro Leu Ile Gln Asn Ser Gly Lys Glu Met Ser
50 55 60

Glu Phe Asp Lys Tyr Gln Gly Leu Ala Asp Val Thr Phe Ser Ile Tyr
65 70 75 80

Asn Val Thr Asn Glu Phe Tyr Glu Gln Arg Ala Ala Gly Ala Ser Val
85 90 95

Asp Ala Ala Lys Gln Ala Val Gln Ser Leu Thr Pro Gly Lys Pro Val
100 105 110

Ala Gln Gly Thr Thr Asp Ala Asn Gly Asn Val Thr Val Gln Leu Pro
115 120 125

Lys Lys Gln Asn Gly Lys Asp Ala Val Tyr Thr Ile Lys Glu Glu Pro
130 135 140

Lys Glu Gly Val Val Ala Ala Thr Asn Met Val Val Ala Phe Pro Val
145 150 155 160

Tyr Glu Met Ile Lys Gln Thr Asp Gly Ser Tyr Lys Tyr Gly Thr Glu
165 170 175

Glu Leu Ala Val Val His Ile Tyr Pro Lys Asn Val Val Ala Asn Asp
180 185 190

Gly Ser Leu His Val Lys Lys Val Gly Thr Ala Glu Asn Glu Gly Leu
195 200 205

Asn Gly Ala Glu Phe Val Ile Ser Lys Ser Glu Gly Ser Pro Gly Thr
210 215 220

Val Lys Tyr Ile Gln Gly Val Lys Asp Gly Leu Tyr Thr Trp Thr Thr
225 230 235 240

Asp Lys Glu Gln Ala Lys Arg Phe Ile Thr Gly Lys Ser Tyr Glu Ile
245 250 255

P07741US01_6-19-06_sequence.txt

Gly Glu Asn Asp Phe Thr Glu Ala Glu Asn Gly Thr Gly Glu Leu Thr
260 265 270

Val Lys Asn Leu Glu Val Gly Ser Tyr Ile Leu Glu Glu Val Lys Ala
275 280 285

Pro Asn Asn Ala Glu Leu Ile Glu Asn Gln Thr Lys Thr Pro Phe Thr
290 295 300

Ile Glu Ala Asn Asn Gln Thr Pro Val Glu Lys Thr Val Lys Asn Asp
305 310 315 320

Thr Ser Lys Val Asp Lys Thr Thr Pro Ser Leu Asp Gly Lys Asp Val
325 330 335

Ala Ile Gly Glu Lys Ile Lys Tyr Gln Ile Ser Val Asn Ile Pro Leu
340 345 350

Gly Ile Ala Asp Lys Glu Gly Asp Ala Asn Lys Tyr Val Lys Phe Asn
355 360 365

Leu Val Asp Lys His Asp Ala Ala Leu Thr Phe Asp Asn Val Thr Ser
370 375 380

Gly Glu Tyr Ala Tyr Ala Leu Tyr Asp Gly Asp Thr Val Ile Ala Pro
385 390 395 400

Glu Asn Tyr Gln Val Thr Glu Gln Ala Asn Gly Phe Thr Val Ala Val
405 410 415

Asn Pro Ala Tyr Ile Pro Thr Leu Thr Pro Gly Gly Thr Leu Lys Phe
420 425 430

Val Tyr Phe Met His Leu Asn Glu Lys Ala Asp Pro Thr Lys Gly Phe
435 440 445

Lys Asn Glu Ala Asn Val Asp Asn Gly His Thr Asp Asp Gln Thr Pro
450 455 460

P07741US01_6-19-06_Sequence.txt

Pro Thr Val Glu Val Val Thr Gly Gly Lys Arg Phe Ile Lys Val Asp
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Gly Asp Val Thr Ala Thr Gln Ala Leu Ala Gly Ala Ser Phe Val Val
485 490 495

Arg Asp Gln Asn Ser Asp Thr Ala Asn Tyr Leu Lys Ile Asp Glu Thr
500 505 510

Thr Lys Ala Ala Thr Trp Val Lys Thr Lys Ala Glu Ala Thr Thr Phe
515 520 525

Thr Thr Thr Ala Asp Gly Leu Val Asp Ile Thr Gly Leu Lys Tyr Gly
530 535 540

Thr Tyr Tyr Leu Glu Glu Thr Val Ala Pro Asp Asp Tyr Val Leu Leu
545 550 555 560

Thr Asn Arg Ile Glu Phe Val Val Asn Glu Gln Ser Tyr Gly Thr Thr
565 570 575

Glu Asn Leu Val Ser Pro Glu Lys Val Pro Asn Lys His Lys Gly Thr
580 585 590

Leu Pro Ser Thr Gly Gly Lys Gly Ile Tyr Val Tyr Leu Gly Ser Gly
595 600 605

Ala Val Leu Leu Leu Ile Ala Gly Val Tyr Phe Ala Arg Arg Arg Lys
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<211> 3387
<212> DNA
<213> Staphylococcus epidermidis

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P07741US01_6-19-06_Sequence.txt

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180

gcgaataaca ccagtgctga aaagatagaa aaagaaattg gtctagtcga aaattactta
240

agtgatgtgg aaagaaaaga aggagatggc tatgcttatac aggtaaatag cgggaaaatt
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acgttggaat tctcatcaaa cactaaacaa actatcgatc tgagttttcc aatcgatcca
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gcactttacc acagccaggc aaacaagctg atcgctcgata ataaagaata tgacattatt
420

gatgagacag aaaataagaa agatacagat gtgtcagtac caaagccaga cgaaatagaa
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gaagaatcat caaaagaaaa cgaaaattct gtcagcccat ttacattgcc tacattatcc
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600

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caaggcaata aaaacggaac aaatcaatgg gatggtataa attcttggaa tggagatcct
720

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780

atacgaaagt atgcaaagga aacaagtaca cccggattgt ttgatgttta tttgaatgct
840

cgtggaaatg tacaaaaaga tatcacgcct cttgatctcg tattgggtcg agactgggtca
900

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960

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1020

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P07741US01_6-19-06_Sequence.txt

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1260

agcaattatt acggaactca gttttctaata acgcaagatc ggccgggaaa tactttctcta
1320

atctcaagaa tctatgatgc acctgaccaa aacaatctat ccagaagaat cgacagtagc
1380

tttatcgcaa ccatcggaga agcgaatggc ctcaaagaac gaggaatcga aatacatggt
1440

cttgatcatc aacttcaaag cgatccggca gctgggtctct caaaagcaga agtagagtct
1500

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1560

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1620

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1680

tcagtcaaga gtgtggggac aagtcctaca acgggtcactc catctatttc catagaagga
1740

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1800

caagtgaaga tccaaacaga aaatgaggac ttccatccaa atttctggta tcaaatgaac
1860

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1920

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1980

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2040

gctgcagctt ggaaaaacgg atatattcga atcattaaac cagctaaaga tacaacaaat
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P07741US01_6-19-06_Sequence.txt

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2280

aaacaattca caccgttaaa cttgaaaata acgaaaaatt cctctacagg tgaaaaggat
2340

cttattggcg ctgttttcaa attaacagga gattctattg atactttact aacagatcat
2400

ggcgacggaa cctattctct tccagaaaat gtcaaattgc aaaaagaaat gacctatacg
2460

ctgacagaaa caaaagctcc agaagggcat ggattaagca aaaagactac ttgggaaatc
2520

aagatcgctt ctgatggtag ggtaaccatt gatggaaaaa cagtcactac ttccgatgat
2580

acgatccagt tgactattga aaatcctttt gttgaagttc ctgtagcagt acgtaagtat
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gcgatgcaag ggacggacaa agagataaat cttaaaggag cagcattttc cctacagaaa
2700

aaagaagcaa atggtactta tcagccaatt gacagccaaa caacgaatga aaaaggctctt
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2820

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2880

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3000

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acagatacct ttctattcga aaatttaaaa cctggaactt atacgctgac cgaaactttt
3120

acaccagaag gataccaagg tctaaaagag ccagttacta tagttataca cgaagatggg
3180

P07741US01_6-19-06_Sequence.txt

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cagatttctt tagacatcac gaatcaggca aaagtaccat tacctgaaac gggaggaatt
3300

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<210> 15

<211> 1129

<212> PRT

<213> Staphylococcus epidermidis

<400> 15

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35 40 45

Gln Ser Gly Lys Lys Ala Leu Asn Ile Lys Leu Asn Ala Asn Asn Thr
50 55 60

Ser Ala Glu Lys Ile Glu Lys Glu Ile Gly Leu Val Glu Asn Tyr Leu
65 70 75 80

Ser Asp Val Glu Arg Lys Glu Gly Asp Gly Tyr Ala Tyr Gln Val Asn
85 90 95

Ser Gly Lys Ile Thr Leu Glu Ile Ser Ser Asn Thr Lys Gln Thr Ile
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Asp Leu Ser Phe Pro Ile Asp Pro Ala Leu Tyr His Ser Gln Ala Asn
115 120 125

P07741US01_6-19-06_Sequence.txt

Lys Leu Ile Val Asp Asn Lys Glu Tyr Asp Ile Ile Asp Glu Thr Glu
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 Asn Lys Lys Asp Thr Asp Val Ser Val Pro Lys Pro Asp Glu Ile Glu
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 Glu Glu Ser Ser Lys Glu Asn Glu Asn Ser Val Ser Pro Phe Thr Leu
 165 170 175
 Pro Thr Leu Ser Leu Pro Ala Val Ser Val Pro Ser Asn Gln Thr Ile
 180 185 190
 Pro Thr Glu Tyr Thr Thr Asp Asp Gln Gly Thr Tyr Pro Lys Ala Ser
 195 200 205
 Trp Gln Pro Thr Gly Asn Thr Asn Val Leu Asp His Gln Gly Asn Lys
 210 215 220
 Asn Gly Thr Asn Gln Trp Asp Gly Ile Asn Ser Trp Asn Gly Asp Pro
 225 230 235 240
 Asn Asp Arg Thr His Ser Tyr Ile Glu Tyr Gly Gly Thr Gly Asn Gln
 245 250 255
 Ala Asp Tyr Ala Ile Arg Lys Tyr Ala Lys Glu Thr Ser Thr Pro Gly
 260 265 270
 Leu Phe Asp Val Tyr Leu Asn Ala Arg Gly Asn Val Gln Lys Asp Ile
 275 280 285
 Thr Pro Leu Asp Leu Val Leu Val Val Asp Trp Ser Gly Ser Met Asn
 290 295 300
 Asp Asn Asn Arg Ile Gly Glu Val Lys Ile Gly Val Asp Arg Phe Val
 305 310 315 320
 Asp Thr Leu Ala Asp Ser Gly Ile Thr Asp Lys Ile Asn Met Gly Tyr
 325 330 335

P07741US01_6-19-06_Sequence.txt

Val Gly Tyr Ser Ser Glu Gly Tyr Ser Tyr Ser Asn Gly Ala Val Gln
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Met Gly Ser Phe Asp Ser Val Lys Asn Gln Val Lys Ser Ile Thr Pro
355 360 365

Ser Arg Thr Asn Gly Gly Thr Phe Thr Gln Lys Ala Leu Arg Asp Ala
370 375 380

Gly Ser Met Leu Ser Val Pro Asn Gly His Lys Lys Val Ile Val Leu
385 390 395 400

Leu Thr Asp Gly Val Pro Thr Phe Ser Tyr Lys Val Gln Arg Val His
405 410 415

Ala Gln Ser Ser Ser Asn Tyr Tyr Gly Thr Gln Phe Ser Asn Thr Gln
420 425 430

Asp Arg Pro Gly Asn Thr Ser Leu Ile Ser Arg Ile Tyr Asp Ala Pro
435 440 445

Asp Gln Asn Asn Leu Ser Arg Arg Ile Asp Ser Thr Phe Ile Ala Thr
450 455 460

Ile Gly Glu Ala Met Ala Leu Lys Glu Arg Gly Ile Glu Ile His Gly
465 470 475 480

Leu Gly Ile Gln Leu Gln Ser Asp Pro Ala Ala Gly Leu Ser Lys Ala
485 490 495

Glu Val Glu Ser Arg Met Arg Gln Met Val Ser Ser Asp Glu Lys Gly
500 505 510

Asp Leu Tyr Tyr Glu Ser Ala Asp His Ala Thr Asp Ile Ser Glu Tyr
515 520 525

Leu Ala Lys Lys Ala Val Gln Ile Ser Ala Thr Val Ser Asn Gly Gln
530 535 540

P07741US01_6-19-06_Sequence.txt

Ile Asn Asp Pro Ile Ala Glu Pro Phe Ile Tyr Gln Pro Gly Thr Leu
545 550 555 560

Ser Val Lys Ser Val Gly Thr Ser Pro Thr Thr Val Thr Pro Ser Ile
565 570 575

Ser Ile Glu Gly Asn Thr Ile Lys Ser Asn Gln Ile Tyr Leu Gly Lys
580 585 590

Asp Gln Glu Ile Gln Ile His Tyr Gln Val Arg Ile Gln Thr Glu Asn
595 600 605

Glu Asp Phe His Pro Asn Phe Trp Tyr Gln Met Asn Gly Arg Thr Thr
610 615 620

Phe Gln Pro Asn Ile Asp Thr Asn Glu Leu Ala Glu Phe Gly Ile Pro
625 630 635 640

Ser Ala Lys Ala Pro Gly Val Ser Leu His Ile Lys Lys Leu Trp Glu
645 650 655

Glu Phe Asp Asn Asn Leu Ala Asp Arg Pro Asp Gln Val Thr Phe Glu
660 665 670

Ile Gln Arg Glu His Thr Thr Asn Ala Ala Ala Trp Lys Asn Gly Tyr
675 680 685

Ile Arg Ile Ile Lys Pro Ala Lys Asp Thr Thr Asn Thr Trp Glu Arg
690 695 700

Ala Asp Ile Asp Lys Leu Ser Ala Asn Ser Gly Glu Ser Tyr Gln Glu
705 710 715 720

Ile Leu Ser Leu Pro Gln Tyr Asn Asn Gln Gly Gln Ala Phe Ser Tyr
725 730 735

Gln Thr Ile Lys Glu Leu Pro Val Pro Gly Tyr Asp Ser Gln Gln Ile
740 745 750

P07741US01_6-19-06_Sequence.txt

Asp Ala Met Thr Trp Lys Asn Thr Lys Gln Phe Thr Pro Leu Asn Leu
755 760 765

Lys Ile Thr Lys Asn Ser Ser Thr Gly Glu Lys Asp Leu Ile Gly Ala
770 775 780

Val Phe Lys Leu Thr Gly Asp Ser Ile Asp Thr Leu Leu Thr Asp His
785 790 795 800

Gly Asp Gly Thr Tyr Ser Leu Pro Glu Asn Val Lys Leu Gln Lys Glu
805 810 815

Met Thr Tyr Thr Leu Thr Glu Thr Lys Ala Pro Glu Gly His Gly Leu
820 825 830

Ser Lys Lys Thr Thr Trp Glu Ile Lys Ile Ala Ser Asp Gly Thr Val
835 840 845

Thr Ile Asp Gly Lys Thr Val Thr Thr Ser Asp Asp Thr Ile Gln Leu
850 855 860

Thr Ile Glu Asn Pro Phe Val Glu Val Pro Val Ala Val Arg Lys Tyr
865 870 875 880

Ala Met Gln Gly Thr Asp Lys Glu Ile Asn Leu Lys Gly Ala Ala Phe
885 890 895

Ser Leu Gln Lys Lys Glu Ala Asn Gly Thr Tyr Gln Pro Ile Asp Ser
900 905 910

Gln Thr Thr Asn Glu Lys Gly Leu Ala Ser Phe Asp Ser Leu Thr Pro
915 920 925

Gly Lys Tyr Arg Val Val Glu Thr Ala Gly Pro Ala Gly Tyr Asp Thr
930 935 940

Ser Pro Gly Asn Tyr Glu Phe Gln Ile Asp Lys Tyr Gly Lys Ile Ile
945 950 955 960

P07741US01_6-19-06_Sequence.txt

Tyr Thr Gly Lys Asn Thr Glu Met Thr Asn Asn Val Trp Thr Leu Thr
965 970 975

His Gln Asn Arg Leu Lys Ala Phe Asp Leu Thr Val His Lys Lys Glu
980 985 990

Asp Asn Gly Gln Thr Leu Lys Gly Ala Lys Phe Arg Leu Gln Gly Pro
995 1000 1005

Glu Met Asp Leu Glu Ser Pro Lys Asp Gly Gln Glu Thr Asp Thr
1010 1015 1020

Phe Leu Phe Glu Asn Leu Lys Pro Gly Thr Tyr Thr Leu Thr Glu
1025 1030 1035

Thr Phe Thr Pro Glu Gly Tyr Gln Gly Leu Lys Glu Pro Val Thr
1040 1045 1050

Ile Val Ile His Glu Asp Gly Ser Ile Gln Val Asp Gly Gln Asp
1055 1060 1065

His Glu Ser Val Leu Ser Pro Gly Ala Lys Asn Asn Gln Ile Ser
1070 1075 1080

Leu Asp Ile Thr Asn Gln Ala Lys Val Pro Leu Pro Glu Thr Gly
1085 1090 1095

Gly Ile Gly Arg Leu Gly Ile Tyr Leu Val Gly Met Ile Gly Cys
1100 1105 1110

Ala Phe Ser Ile Trp Tyr Leu Phe Leu Lys Lys Glu Arg Gly Gly
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Ser

<210> 16
<211> 1422
<212> DNA

<213> Staphylococcus epidermidis

<400> 16

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P07741US01_6-19-06_Sequence.txt

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1080

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1140

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1200

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1320

acaaacgaaa cgaaaaatac acttttaggc gttgttggtg tggtattcgc aagctttgca
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<210> 17

<211> 473

<212> PRT

<213> Staphylococcus epidermidis

<400> 17

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35 40 45

Asn His Pro Asn Asp Gly Gln Glu Lys Ala Leu Leu Gln Thr Tyr Arg
50 55 60

Gly Leu Asn Gly Val Thr Phe Gln Val Tyr Asp Val Thr Asp Ser Phe
65 70 75 80

Tyr His Leu Arg Glu Lys Gly Lys Thr Val Glu Glu Ala Gln Ala Glu
Page 56

Ile Ala Lys Asn Gly Ala Ser Ser Gly Met Phe Thr Ala Glu Ala Thr
 100 105 110

Thr Thr Thr Leu Asn Asn Glu Asp Gly Ile Ala Ser Phe Ser Leu Ala
 115 120 125

Ala Lys Asp Gln Glu Lys Arg Asp Lys Ala Tyr Leu Phe Ile Glu Ser
 130 135 140

Lys Val Pro Glu Val Val Lys Glu Lys Ala Glu Asn Met Val Val Val
 145 150 155 160

Leu Pro Val His Gly Gln Asn Asn Gln Lys Leu Ser Thr Ile His Leu
 165 170 175

Tyr Pro Lys Asn Glu Glu Asn Asp Tyr Pro Asp Pro Pro Phe Glu Lys
 180 185 190

Val Leu Glu Glu Pro Arg Asn Asp Phe Thr Ile Gly Glu Lys Ile Thr
 195 200 205

Tyr Ser Leu His Thr Thr Ile Pro Val Asn Ile Leu Asp Tyr Gln Lys
 210 215 220

Phe Glu Leu Ser Asp Ser Ala Asp Glu Ala Leu Thr Phe Leu Pro Asn
 225 230 235 240

Ser Leu Thr Ile Ser Ser Asn Gly Glu Lys Leu Thr Glu Gly Phe Val
 245 250 255

Ile His Lys Lys Pro His Gly Phe Asp Val Leu Phe Ser Ile Pro Ser
 260 265 270

Leu Glu Lys Tyr Ala Gly Lys Lys Leu Thr Ile Ser Tyr Gln Met Gln
 275 280 285

Leu Ser Ser Thr Ala Gln Ala Asn Lys Glu Ile Asn Asn Asn Gly Thr
 Page 57

290

295

300

Leu Asp Phe Gly Phe Gly Val Ser Thr Lys Lys Val Ser Val Tyr Thr
305 310 315 320

Gly Ser Lys Gln Phe Val Lys Ile Glu Thr Asn Lys Pro Asp Lys Arg
325 330 335

Leu Ala Gly Ala Val Phe Leu Ile Lys Asn Lys Ala Gly Asn Tyr Leu
340 345 350

Gln Gln Thr Ala Asn Gly Tyr Lys Trp Thr Lys Asn Glu Ser Asp Ala
355 360 365

Leu His Leu Ile Ser Asp Lys Asn Gly Ala Phe Ser Ile Ser Gly Leu
370 375 380

Lys Thr Gly Ser Tyr Arg Leu Lys Glu Ile Glu Ala Pro Ser Gly Tyr
385 390 395 400

Ile Leu Ser Glu Thr Glu Ile Pro Phe Thr Ile Ser Thr Phe Leu Ser
405 410 415

Glu Asp Lys Glu Ala Asp Ser Ile Leu Lys Val Val Asn Lys Lys Glu
420 425 430

Asn Ser Arg Pro Phe Leu Pro Lys Thr Asn Glu Thr Lys Asn Thr Leu
435 440 445

Leu Gly Val Val Gly Met Val Phe Ala Ser Phe Ala Ile Trp Leu Phe
450 455 460

Ile Lys Lys Arg Thr Gly Val Lys Lys
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<210> 18

<211> 1878

<212> DNA

<213> Staphylococcus epidermidis

P07741US01_6-19-06_Sequence.txt

<400> 18

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ctcacaaaca gcttcggcgc aaaaaaagtg tttgcagagg agacagcagc tcaagtcatc
120

cttcataaaa agaaaatgac tgattttaccc gatcctttaa tccaaaacag cgggaaagaa
180

atgagcgaat tcgatcaata ccaaggatta gccgatattt cattttcagt ttataacgtc
240

actcaagaat tttatgcgca acgagataaa ggagcgtccg tggatgcagc aaaacaagca
300

gtccagtctt tgactcctgg tacaccagtt gcttcaggaa cgacagatgc tgatggaaat
360

gtcactttat ctttacctaa aaaacaaaat gggaaagatg cagtctacac gatcaaagaa
420

gaaccaaaaag acggagtgtc agctgccgca aacatggttt tagctttccc tgtatatgag
480

atgatcaaac aagcagatgg ctcttataaa tacgggacag aagaactaga tactatccat
540

ctctacccta aaaatacagt cggtaatgat ggaacgttga aagttacaaa aatcggtact
600

gccgaaaacg aagcactaaa tggagcagaa tttattattt ctaaagaaga aggaacacca
660

agcgtcaaaa aatacatcca aagtgtcaca gatggattgt acacttggac aactgatcaa
720

accaaagcca aacatttcat tactggtcat tcttatgaca tcggcaacaa tgactttgcc
780

gaggcatcta ttgaaaaagg ccagttgatc gttaatcatt tagaagttgg aaaatataat
840

ttagaagaag taaaagctcc tgataatgcg gaaatgattg aaaagcaaac aatcacgcct
900

tttgagatcc tggcaaatac ccaaacacca gtagaaaaga ccatcaaaaa tgatacgtct
960

aaagttgata aaacaacacc tcaattgaat ggaaaagatg tcgcaatcgg tgaaaaaatt
1020

P07741US01_6-19-06_Sequence.txt

caatatgaga tttctgtcaa tatcccatta ggtatcgctg ataaagaagg aacgcaaaac
1080

aagtacacaa cattcaaact tatcgatact catgacgctg ctttaacatt tgataatgat
1140

tcttcaggaa cgtatgctta tgccttatat gatggaaata aagaaatcga cccagtaaatt
1200

tattctgtca ctgagcaaac agacggattc acggtttcag ttgatccgaa ttatattcct
1260

tcattaactc ctggcgggtac attgaaattc gtttactata tgcatttgaa cgaaaaagca
1320

gatccaacca aaggattttc taaccaagca aatgtcgata acgggcatac aaatgatcaa
1380

acaccaccgt cagtcgatgt cgttactggg ggcaaacgat ttgttaaagt agatggtgac
1440

gttacatcag accaaacact tgctggagca gaattcgtcg ttcgtgatca agatagtgac
1500

acagcgaaat atttatcgat cgacccatcc acaaaagccg tcagctgggt atcggcgaaa
1560

gaatcagcaa cggtttttac aaccacaagt aacggtttaa tcgatgtgac aggtctaaaa
1620

tatggcacgt actatctgga agaaacgaaa gcgccagaaa aatatgttcc attaacaaac
1680

cgtgtagcat ttactatcga tgaacaatct tatgtaacag caggacagtt gatttctcct
1740

gaaaaaatac caaataaaca caaagggtaca cttccttcaa caggcggtaa gggaaatctat
1800

gtgtatatcg gtgcaggagt agtccttcta ctgattgctg gactgtactt tgctagacgc
1860

aagcacagtc agatttag
1878

<210> 19

<211> 625

<212> PRT

<213> Staphylococcus epidermidis

<400> 19

P07741US01_6-19-06_Sequence.txt

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Met Lys Asn His Lys Lys Ile Asn Val Met Leu Gly Val Leu Phe Leu
1          5          10          15

Ile Leu Pro Leu Leu Thr Asn Ser Phe Gly Ala Lys Lys Val Phe Ala
          20          25          30

Glu Glu Thr Ala Ala Gln Val Ile Leu His Lys Lys Lys Met Thr Asp
          35          40          45

Leu Pro Asp Pro Leu Ile Gln Asn Ser Gly Lys Glu Met Ser Glu Phe
          50          55          60

Asp Gln Tyr Gln Gly Leu Ala Asp Ile Ser Phe Ser Val Tyr Asn Val
65          70          75          80

Thr Gln Glu Phe Tyr Ala Gln Arg Asp Lys Gly Ala Ser Val Asp Ala
          85          90          95

Ala Lys Gln Ala Val Gln Ser Leu Thr Pro Gly Thr Pro Val Ala Ser
          100          105          110

Gly Thr Thr Asp Ala Asp Gly Asn Val Thr Leu Ser Leu Pro Lys Lys
          115          120          125

Gln Asn Gly Lys Asp Ala Val Tyr Thr Ile Lys Glu Glu Pro Lys Asp
          130          135          140

Gly Val Ser Ala Ala Ala Asn Met Val Leu Ala Phe Pro Val Tyr Glu
145          150          155          160

Met Ile Lys Gln Ala Asp Gly Ser Tyr Lys Tyr Gly Thr Glu Glu Leu
          165          170          175

Asp Thr Ile His Leu Tyr Pro Lys Asn Thr Val Gly Asn Asp Gly Thr
          180          185          190

Leu Lys Val Thr Lys Ile Gly Thr Ala Glu Asn Glu Ala Leu Asn Gly
          195          200          205

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P07741US01_6-19-06_Sequence.txt

Ala Glu Phe Ile Ile Ser Lys Glu Glu Gly Thr Pro Ser Val Lys Lys
210 215 220

Tyr Ile Gln Ser Val Thr Asp Gly Leu Tyr Thr Trp Thr Thr Asp Gln
225 230 235 240

Thr Lys Ala Lys His Phe Ile Thr Gly His Ser Tyr Asp Ile Gly Asn
245 250 255

Asn Asp Phe Ala Glu Ala Ser Ile Glu Lys Gly Gln Leu Ile Val Asn
260 265 270

His Leu Glu Val Gly Lys Tyr Asn Leu Glu Glu Val Lys Ala Pro Asp
275 280 285

Asn Ala Glu Met Ile Glu Lys Gln Thr Ile Thr Pro Phe Glu Ile Leu
290 295 300

Ala Asn Ser Gln Thr Pro Val Glu Lys Thr Ile Lys Asn Asp Thr Ser
305 310 315 320

Lys Val Asp Lys Thr Thr Pro Gln Leu Asn Gly Lys Asp Val Ala Ile
325 330 335

Gly Glu Lys Ile Gln Tyr Glu Ile Ser Val Asn Ile Pro Leu Gly Ile
340 345 350

Ala Asp Lys Glu Gly Thr Gln Asn Lys Tyr Thr Thr Phe Lys Leu Ile
355 360 365

Asp Thr His Asp Ala Ala Leu Thr Phe Asp Asn Asp Ser Ser Gly Thr
370 375 380

Tyr Ala Tyr Ala Leu Tyr Asp Gly Asn Lys Glu Ile Asp Pro Val Asn
385 390 395 400

Tyr Ser Val Thr Glu Gln Thr Asp Gly Phe Thr Val Ser Val Asp Pro
405 410 415

P07741US01_6-19-06_Sequence.txt

```

Asn Tyr Ile Pro Ser Leu Thr Pro Gly Gly Thr Leu Lys Phe Val Tyr
      420      425      430

Tyr Met His Leu Asn Glu Lys Ala Asp Pro Thr Lys Gly Phe Ser Asn
      435      440      445

Gln Ala Asn Val Asp Asn Gly His Thr Asn Asp Gln Thr Pro Pro Ser
      450      455      460

Val Asp Val Val Thr Gly Gly Lys Arg Phe Val Lys Val Asp Gly Asp
      465      470      475      480

Val Thr Ser Asp Gln Thr Leu Ala Gly Ala Glu Phe Val Val Arg Asp
      485      490      495

Gln Asp Ser Asp Thr Ala Lys Tyr Leu Ser Ile Asp Pro Ser Thr Lys
      500      505      510

Ala Val Ser Trp Val Ser Ala Lys Glu Ser Ala Thr Val Phe Thr Thr
      515      520      525

Thr Ser Asn Gly Leu Ile Asp Val Thr Gly Leu Lys Tyr Gly Thr Tyr
      530      535      540

Tyr Leu Glu Glu Thr Lys Ala Pro Glu Lys Tyr Val Pro Leu Thr Asn
      545      550      555      560

Arg Val Ala Phe Thr Ile Asp Glu Gln Ser Tyr Val Thr Ala Gly Gln
      565      570      575

Leu Ile Ser Pro Glu Lys Ile Pro Asn Lys His Lys Gly Thr Leu Pro
      580      585      590

Ser Thr Gly Gly Lys Gly Ile Tyr Val Tyr Ile Gly Ala Gly Val Val
      595      600      605

Leu Leu Leu Ile Ala Gly Leu Tyr Phe Ala Arg Arg Lys His Ser Gln
      610      615      620

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P07741US01_6-19-06_Sequence.txt

Ile
625

<210> 20
<211> 2402
<212> PRT
<213> Staphylococcus epidermidis

<400> 20

Met Lys Asn Lys Gln Gly Phe Leu Pro Asn Leu Leu Asn Lys Tyr Gly
1 5 10 15

Ile Arg Lys Leu Ser Ala Gly Thr Ala Ser Leu Leu Ile Gly Ala Thr
20 25 30

Leu Val Phe Gly Ile Asn Gly Gln Val Lys Ala Ala Glu Thr Asp Asn
35 40 45

Ile Val Ser Gln Asn Gly Asp Asn Lys Thr Asn Asp Ser Glu Ser Ser
50 55 60

Asp Lys Glu Leu Val Lys Ser Glu Asp Asp Lys Thr Ser Ser Thr Ser
65 70 75 80

Thr Asp Thr Asn Leu Glu Ser Glu Phe Asp Gln Asn Asn Asn Pro Ser
85 90 95

Ser Ile Glu Glu Ser Thr Asn Arg Asn Asp Glu Asp Thr Leu Asn Gln
100 105 110

Arg Thr Ser Thr Glu Thr Glu Lys Asp Thr His Val Lys Ser Ala Asp
115 120 125

Thr Gln Thr Thr Asn Glu Thr Thr Asn Lys Asn Asp Asp Asn Ala Thr
130 135 140

Thr Asn His Thr Glu Ser Ile Ser Asp Glu Ser Thr Tyr Gln Ser Asp
145 150 155 160

P07741US01_6-19-06_Sequence.txt

Asp Ser Lys Thr Thr Gln His Asp Asn Ser Asn Thr Asn Gln Asp Thr
165 170 175

Gln Ser Thr Leu Asn Pro Thr Ser Lys Glu Ser Ser Asn Lys Asp Glu
180 185 190

Ala Thr Ser Pro Thr Pro Lys Glu Ser Thr Ser Ile Glu Lys Thr Asn
195 200 205

Leu Ser Asn Asp Ala Asn His Gln Thr Thr Asp Glu Val Asn His Ser
210 215 220

Asp Ser Asp Asn Met Thr Asn Ser Thr Pro Asn Asp Thr Glu Asn Glu
225 230 235 240

Leu Asp Thr Thr Gln Leu Thr Ser His Asp Glu Ser Pro Ser Pro Gln
245 250 255

Ser Asp Asn Phe Thr Gly Phe Thr Asn Leu Met Ala Thr Pro Leu Asn
260 265 270

Leu Arg Asn Asp Asn Pro Arg Ile Asn Leu Leu Ala Ala Thr Glu Asp
275 280 285

Thr Lys Pro Lys Thr Tyr Lys Lys Pro Asn Asn Ser Glu Tyr Ser Tyr
290 295 300

Leu Leu Asn Asp Leu Gly Tyr Asp Ala Thr Thr Val Lys Glu Asn Ser
305 310 315 320

Asp Leu Arg His Ala Gly Ile Ser Gln Ser Gln Asp Asn Thr Gly Ser
325 330 335

Val Ile Lys Leu Asn Leu Thr Lys Trp Leu Ser Leu Gln Ser Asp Phe
340 345 350

Val Asn Gly Gly Lys Val Asn Leu Ser Phe Ala Gln Ser Asp Phe Tyr
355 360 365

P07741US01_6-19-06_Sequence.txt

Thr Gln Ile Glu Ser Ile Thr Leu Asn Asp Val Lys Met Asp Thr Thr
370 375 380

Asn Asn Gly Gln Asn Trp Ser Ala Pro Ile Asn Gly Ser Thr Val Arg
385 390 395 400

Ser Gly Leu Ile Gly Ser Val Thr Asn His Asp Ile Val Ile Thr Leu
405 410 415

Lys Asn Ser Gln Thr Leu Ser Ser Leu Gly Tyr Ser Asn Asn Lys Pro
420 425 430

Val Tyr Leu Thr His Thr Trp Thr Thr Asn Asp Gly Ala Ile Ala Glu
435 440 445

Glu Ser Ile Gln Val Ala Ser Ile Thr Pro Thr Leu Asp Ser Lys Ala
450 455 460

Pro Asn Thr Ile Gln Lys Ser Asp Phe Thr Ala Gly Arg Met Thr Asn
465 470 475 480

Lys Ile Lys Tyr Asp Ser Ser Gln Asn Ser Ile Lys Ser Val His Thr
485 490 495

Phe Lys Pro Asn Glu Asn Phe Leu Gln Thr Asp Tyr Arg Ala Val Leu
500 505 510

Tyr Ile Lys Glu Gln Val Asn Lys Glu Leu Ile Pro Tyr Ile Asp Pro
515 520 525

Asn Ser Val Lys Leu Tyr Val Ser Asp Pro Asp Gly Asn Pro Ile Ser
530 535 540

Gln Asp Arg Tyr Val Asn Gly Ser Ile Asp Asn Asp Gly Leu Phe Asp
545 550 555 560

Ser Ser Lys Ile Asn Glu Ile Ser Ile Lys Asn Asn Asn Thr Ser Gly
565 570 575

P07741US01_6-19-06_Sequence.txt

Gln Leu Ser Asn Ala Arg Thr Ser Leu Asp Arg Asn Val Phe Phe Gly
580 585 590

Thr Leu Gly Gln Ser Arg Ser Tyr Thr Ile Ser Tyr Lys Leu Lys Asp
595 600 605

Gly Tyr Thr Leu Glu Ser Val Ala Ser Lys Val Ser Ala Arg Glu Thr
610 615 620

Phe Asp Ser Trp Met Glu Val Asp Tyr Leu Asp Ser Tyr Asp Ser Gly
625 630 635 640

Ala Pro Asn Lys Arg Leu Leu Gly Ser Tyr Ala Ser Ser Tyr Ile Asp
645 650 655

Met Ile Asp Arg Ile Pro Pro Val Ala Pro Lys Ala Asn Ser Ile Thr
660 665 670

Thr Glu Asp Thr Ser Ile Lys Gly Thr Ala Glu Val Asp Thr Asn Ile
675 680 685

Asn Leu Thr Phe Asn Asp Gly Arg Thr Leu Asn Gly Lys Val Asp Ser
690 695 700

Asn Gly Asn Phe Ser Ile Ala Ile Pro Ser Tyr Tyr Val Leu Thr Gly
705 710 715 720

Lys Glu Thr Ile Lys Ile Thr Ser Ile Asp Lys Gly Asp Asn Val Ser
725 730 735

Pro Ala Ile Thr Ile Ser Val Ile Asp Lys Thr Pro Pro Ala Val Lys
740 745 750

Ala Ile Ser Asn Lys Thr Gln Lys Val Asn Thr Glu Ile Glu Pro Ile
755 760 765

Lys Ile Glu Ala Thr Asp Asn Ser Gly Gln Ala Val Thr Asn Lys Val
770 775 780

P07741US01_6-19-06_sequence.txt

Glu Gly Leu Pro Ala Gly Met Thr Phe Asp Glu Ala Thr Asn Thr Ile
 785 790 795 800
 Ser Gly Thr Pro Ser Glu Val Gly Ser Tyr Asp Ile Thr Val Thr Thr
 805 810 815
 Thr Asp Glu Asn Gly Asn Ser Glu Thr Thr Thr Phe Thr Ile Asp Val
 820 825 830
 Glu Asp Thr Thr Lys Pro Thr Val Glu Ser Val Ala Asp Gln Thr Gln
 835 840 845
 Glu Val Asn Thr Glu Ile Glu Pro Ile Lys Ile Glu Ala Thr Asp Asn
 850 855 860
 Ser Gly Arg Ala Val Thr Asn Lys Val Asp Gly Leu Pro Asp Gly Val
 865 870 875 880
 Thr Phe Asp Glu Ala Thr Asn Thr Ile Ser Gly Thr Pro Ser Glu Val
 885 890 895
 Gly Ser Tyr Asp Ile Thr Val Thr Thr Thr Asp Glu Ser Gly Asn Val
 900 905 910
 Thr Glu Thr Ile Phe Thr Ile Asp Val Glu Asp Thr Thr Lys Pro Thr
 915 920 925
 Val Glu Ser Ile Ala Gly Gln Thr Gln Glu Val Asn Thr Glu Ile Glu
 930 935 940
 Pro Ile Lys Ile Glu Ala Lys Asp Asn Ser Gly Gln Thr Val Thr Asn
 945 950 955 960
 Lys Val Asp Gly Leu Pro Asp Gly Val Thr Phe Asp Glu Ala Thr Asn
 965 970 975
 Thr Ile Ser Gly Thr Pro Ser Glu Val Gly Ser Tyr Asp Val Thr Val
 980 985 990

P07741US01_6-19-06_sequence.txt

Thr Thr Thr Asp Glu Ser Gly Asn Ser Glu Thr Thr Thr Phe Thr Ile
995 1000 1005

Glu Val Lys Asp Thr Thr Lys Pro Thr Val Glu Ser Val Ala Asp
1010 1015 1020

Gln Thr Gln Glu Val Asn Thr Glu Ile Glu Pro Ile Lys Ile Glu
1025 1030 1035

Ala Arg Asp Asn Ser Gly Gln Ala Val Thr Asn Lys Val Asp Gly
1040 1045 1050

Leu Pro Asp Gly Val Thr Phe Asp Glu Ala Thr Asn Thr Ile Ser
1055 1060 1065

Gly Thr Pro Ser Glu Val Gly Ser Tyr Asp Ile Thr Val Thr Thr
1070 1075 1080

Thr Asp Glu Ser Gly Asn Val Thr Glu Thr Thr Phe Thr Ile Glu
1085 1090 1095

Val Glu Asp Thr Thr Lys Pro Thr Val Glu Asn Val Ala Asp Gln
1100 1105 1110

Thr Gln Glu Val Asn Thr Glu Ile Thr Pro Ile Thr Ile Glu Ser
1115 1120 1125

Glu Asp Asn Ser Gly Gln Thr Val Thr Asn Lys Val Asp Gly Leu
1130 1135 1140

Pro Asp Gly Val Thr Phe Asp Glu Thr Thr Asn Thr Ile Ser Gly
1145 1150 1155

Thr Pro Ser Lys Val Gly Ser Tyr Asp Ile Thr Val Thr Thr Thr
1160 1165 1170

Asp Glu Ser Gly Asn Ala Thr Glu Thr Thr Phe Thr Ile Glu Val
1175 1180 1185

P07741US01_6-19-06_Sequence.txt

Glu	Asp	Thr	Thr	Lys	Pro	Thr	Val	Glu	Asn	Val	Ala	Gly	Gln	Thr
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Gln	Glu	Ile	Asn	Thr	Glu	Ile	Glu	Pro	Ile	Lys	Ile	Glu	Ala	Thr
1205						1210					1215			
Asp	Asn	Ser	Gly	Gln	Ala	Val	Thr	Asn	Lys	Val	Glu	Gly	Leu	Pro
1220						1225					1230			
Ala	Gly	Val	Thr	Phe	Asp	Glu	Ala	Thr	Asn	Thr	Ile	Ser	Gly	Thr
1235						1240					1245			
Pro	Ser	Glu	Val	Gly	Ser	Tyr	Thr	Val	Thr	Val	Thr	Thr	Met	Asp
1250						1255					1260			
Glu	Ser	Gly	Asn	Ala	Thr	Glu	Thr	Thr	Phe	Thr	Ile	Asp	Val	Glu
1265						1270					1275			
Asp	Thr	Thr	Lys	Pro	Thr	Val	Glu	Ser	Val	Ala	Asp	Gln	Thr	Gln
1280						1285					1290			
Glu	Val	Asn	Thr	Glu	Ile	Thr	Pro	Ile	Thr	Ile	Glu	Ser	Glu	Asp
1295						1300					1305			
Asn	Ser	Asp	Gln	Ala	Val	Thr	Asn	Lys	Val	Asp	Gly	Leu	Pro	Asp
1310						1315					1320			
Gly	Val	Thr	Phe	Asp	Glu	Ala	Thr	Asn	Thr	Ile	Ser	Gly	Thr	Pro
1325						1330					1335			
Ser	Glu	Val	Gly	Ser	Tyr	Thr	Val	Thr	Val	Thr	Thr	Thr	Asp	Glu
1340						1345					1350			
Ser	Gly	Asn	Ala	Thr	Glu	Thr	Thr	Phe	Thr	Ile	Asp	Val	Glu	Asp
1355						1360					1365			
Thr	Thr	Lys	Pro	Thr	Val	Lys	Ser	Val	Ser	Asp	Gln	Thr	Gln	Glu
1370						1375					1380			

P07741US01_6-19-06_Sequence.txt

Val	Asn	Thr	Glu	Ile	Thr	Pro	Ile	Lys	Ile	Glu	Ala	Thr	Asp	Asn
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Ser	Gly	Gln	Thr	Val	Thr	Asn	Lys	Val	Asp	Gly	Leu	Pro	Asp	Gly
1400						1405					1410			
Ile	Thr	Phe	Asp	Glu	Ala	Thr	Asn	Thr	Ile	Ser	Gly	Thr	Pro	Ser
1415						1420					1425			
Glu	Val	Gly	Ser	Tyr	Asp	Ile	Thr	Val	Thr	Thr	Thr	Asp	Glu	Ser
1430						1435					1440			
Gly	Asn	Ala	Thr	Glu	Thr	Thr	Phe	Thr	Ile	Asn	Val	Glu	Asp	Thr
1445						1450					1455			
Thr	Lys	Pro	Thr	Val	Glu	Asp	Ile	Ala	Asp	Gln	Thr	Gln	Glu	Val
1460						1465					1470			
Asn	Thr	Glu	Ile	Glu	Pro	Ile	Lys	Ile	Glu	Ala	Thr	Asp	Asn	Gly
1475						1480					1485			
Gly	Gln	Ala	Val	Thr	Asn	Lys	Val	Asp	Gly	Leu	Pro	Asp	Gly	Val
1490						1495					1500			
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1505						1510					1515			
Val	Gly	Ser	Tyr	Asp	Ile	Ile	Val	Thr	Thr	Thr	Asp	Glu	Asn	Gly
1520						1525					1530			
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1535						1540					1545			
Lys	Pro	Thr	Val	Glu	Ser	Val	Val	Asp	Gln	Thr	Gln	Glu	Val	Asn
1550						1555					1560			
Thr	Glu	Ile	Thr	Pro	Ile	Lys	Ile	Glu	Ala	Thr	Asp	Asn	Ser	Gly
1565						1570					1575			

P07741US01_6-19-06_Sequence.txt

Gln	Ala	Val	Ala	Asn	Lys	Val	Asp	Gly	Leu	Pro	Asn	Gly	Val	Thr
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Phe	Asp	Glu	Thr	Thr	Asn	Thr	Ile	Ser	Gly	Thr	Pro	Ser	Glu	Val
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Gly	Ser	Tyr	Asp	Ile	Ile	Val	Thr	Thr	Thr	Asp	Glu	Ser	Gly	Asn
1610						1615					1620			
Val	Thr	Glu	Thr	Ile	Phe	Thr	Ile	Asp	Val	Glu	Asp	Thr	Thr	Lys
1625						1630					1635			
Pro	Thr	Val	Glu	Ser	Ile	Ala	Gly	Gln	Thr	Gln	Glu	Val	Asn	Thr
1640						1645					1650			
Glu	Ile	Glu	Pro	Ile	Lys	Ile	Glu	Ala	Thr	Asp	Asn	Ser	Gly	Gln
1655						1660					1665			
Ala	Val	Thr	Asn	Lys	Val	Asp	Gly	Leu	Pro	Asn	Gly	Val	Thr	Phe
1670						1675					1680			
Asp	Glu	Ala	Thr	Asn	Thr	Ile	Ser	Gly	Thr	Pro	Ser	Glu	Val	Gly
1685						1690					1695			
Ile	Tyr	Thr	Val	Thr	Val	Thr	Thr	Thr	Asp	Glu	Ser	Gly	Asn	Ala
1700						1705					1710			
Thr	Glu	Thr	Thr	Phe	Thr	Ile	Asp	Val	Glu	Asp	Thr	Thr	Lys	Pro
1715						1720					1725			
Thr	Val	Glu	Ser	Val	Ala	Asp	Gln	Thr	Gln	Glu	Val	Asn	Thr	Glu
1730						1735					1740			
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1745						1750					1755			
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1760						1765					1770			

P07741US01_6-19-06_Sequence.txt

Glu	Thr	Thr	Asn	Thr	Ile	Ser	Gly	Thr	Pro	Ser	Glu	Val	Gly	Ser
1775						1780					1785			
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1790						1795					1800			
Glu	Thr	Thr	Phe	Thr	Ile	Asp	Val	Glu	Asp	Thr	Thr	Lys	Pro	Thr
1805						1810					1815			
Val	Glu	Ser	Ile	Ala	Asn	Gln	Thr	Gln	Glu	Val	Asn	Thr	Glu	Ile
1820						1825					1830			
Thr	Pro	Ile	Lys	Ile	Glu	Ala	Thr	Asp	Asn	Ser	Gly	Gln	Ala	Val
1835						1840					1845			
Thr	Asn	Lys	Val	Asp	Gly	Leu	Pro	Asn	Gly	Val	Thr	Phe	Asp	Glu
1850						1855					1860			
Thr	Thr	Asn	Thr	Ile	Ser	Gly	Thr	Pro	Ser	Glu	Val	Gly	Ser	Tyr
1865						1870					1875			
Asp	Ile	Lys	Val	Thr	Thr	Thr	Asp	Glu	Ser	Gly	Asn	Ala	Thr	Glu
1880						1885					1890			
Thr	Thr	Phe	Thr	Ile	Asn	Val	Glu	Asp	Thr	Thr	Lys	Pro	Thr	Val
1895						1900					1905			
Glu	Ser	Val	Ala	Asp	Gln	Thr	Gln	Glu	Ile	Asn	Thr	Glu	Ile	Glu
1910						1915					1920			
Pro	Ile	Lys	Ile	Glu	Ala	Arg	Asp	Asn	Ser	Gly	Gln	Ala	Val	Thr
1925						1930					1935			
Asn	Lys	Val	Asp	Gly	Leu	Pro	Asp	Gly	Val	Thr	Phe	Asp	Glu	Ala
1940						1945					1950			
Thr	Asn	Thr	Ile	Ser	Gly	Thr	Pro	Ser	Glu	Val	Gly	Ser	Tyr	Asp
1955						1960					1965			

P07741US01_6-19-06_Sequence.txt

Ile	Thr	Val	Thr	Thr	Thr	Asp	Glu	Ser	Gly	Asn	Ala	Thr	Glu	Thr
1970						1975					1980			
Thr	Phe	Thr	Ile	Asp	Val	Glu	Asp	Thr	Thr	Lys	Pro	Thr	Val	Glu
1985						1990					1995			
Asp	Ile	Thr	Asp	Gln	Thr	Gln	Glu	Ile	Asn	Thr	Glu	Met	Thr	Pro
2000						2005					2010			
Ile	Lys	Ile	Glu	Ala	Thr	Asp	Asn	Ser	Gly	Gln	Ala	Val	Thr	Asn
2015						2020					2025			
Lys	Val	Glu	Gly	Leu	Pro	Asp	Gly	Val	Thr	Phe	Asp	Glu	Ala	Thr
2030						2035					2040			
Asn	Thr	Ile	Ser	Gly	Thr	Pro	Ser	Glu	Val	Gly	Lys	Tyr	Leu	Ile
2045						2050					2055			
Thr	Ile	Thr	Thr	Ile	Asp	Lys	Asp	Gly	Asn	Thr	Ala	Thr	Thr	Thr
2060						2065					2070			
Leu	Thr	Ile	Asn	Val	Ile	Asp	Thr	Thr	Thr	Pro	Glu	Gln	Pro	Thr
2075						2080					2085			
Ile	Asn	Lys	Val	Thr	Glu	Asn	Ser	Thr	Glu	Val	Asn	Gly	Arg	Gly
2090						2095					2100			
Glu	Pro	Gly	Thr	Val	Val	Glu	Val	Thr	Phe	Pro	Asp	Gly	Asn	Lys
2105						2110					2115			
Val	Glu	Gly	Lys	Val	Asp	Ser	Asp	Gly	Asn	Tyr	His	Ile	Gln	Ile
2120						2125					2130			
Pro	Ser	Glu	Thr	Thr	Leu	Lys	Gly	Gly	Gln	Pro	Leu	Gln	Val	Ile
2135						2140					2145			
Ala	Ile	Asp	Lys	Ala	Gly	Asn	Lys	Ser	Glu	Ala	Thr	Thr	Thr	Asn
2150						2155					2160			

P07741US01_6-19-06_Sequence.txt

Val	Ile	Asp	Thr	Thr	Ala	Pro	Glu	Gln	Pro	Thr	Ile	Asn	Lys	Val
2165						2170					2175			
Thr	Glu	Asn	Ser	Thr	Glu	Val	Ser	Gly	Arg	Gly	Glu	Pro	Gly	Thr
2180						2185					2190			
Val	Val	Glu	Val	Thr	Phe	Pro	Asp	Gly	Asn	Lys	Val	Glu	Gly	Lys
2195						2200					2205			
Val	Asp	Ser	Asp	Gly	Asn	Tyr	His	Ile	Gln	Ile	Pro	Ser	Asp	Glu
2210						2215					2220			
Arg	Phe	Lys	Val	Gly	Gln	Gln	Leu	Ile	Val	Lys	Val	Val	Asp	Glu
2225						2230					2235			
Glu	Gly	Asn	Val	Ser	Glu	Pro	Ser	Ile	Thr	Met	Val	Gln	Lys	Glu
2240						2245					2250			
Asp	Lys	Asn	Ser	Glu	Lys	Leu	Ser	Thr	Val	Thr	Gly	Thr	Val	Thr
2255						2260					2265			
Lys	Asn	Asn	Ser	Lys	Ser	Leu	Lys	His	Lys	Ala	Ser	Glu	Gln	Gln
2270						2275					2280			
Ser	Tyr	His	Asn	Lys	Ser	Glu	Lys	Ile	Lys	Asn	Val	Asn	Lys	Pro
2285						2290					2295			
Thr	Lys	Ile	Val	Glu	Lys	Asp	Met	Ser	Thr	Tyr	Asp	Tyr	Ser	Arg
2300						2305					2310			
Tyr	Ser	Lys	Asp	Ile	Ser	Asn	Lys	Asn	Asn	Lys	Ser	Ala	Thr	Phe
2315						2320					2325			
Glu	Gln	Gln	Asn	Val	Ser	Asp	Ile	Asn	Asn	Asn	Gln	Tyr	Ser	Arg
2330						2335					2340			
Asn	Lys	Val	Asn	Gln	Pro	Val	Lys	Lys	Ser	Arg	Lys	Asn	Glu	Ile
2345						2350					2355			

P07741US01_6-19-06_Sequence.txt

Asn Lys Asp Leu Pro Gln Thr Gly Glu Glu Asn Phe Asn Lys Ser
2360 2365 2370

Thr Leu Phe Gly Thr Leu Val Ala Ser Leu Gly Ala Leu Leu Leu
2375 2380 2385

Phe Phe Lys Arg Arg Lys Lys Asp Glu Asn Asp Glu Lys Glu
2390 2395 2400

<210> 21
<211> 892
<212> PRT
<213> Staphylococcus epidermidis

<400> 21

Leu Phe Gly Leu Gly His Asn Glu Ala Lys Ala Glu Glu Asn Thr Val
1 5 10 15

Gln Asp Val Lys Asp Ser Asn Met Asp Asp Glu Leu Ser Asp Ser Asn
20 25 30

Asp Gln Ser Ser Asn Glu Glu Lys Asn Asp Val Ile Asn Asn Ser Gln
35 40 45

Ser Ile Asn Thr Asp Asp Asp Asn Gln Ile Lys Lys Glu Glu Thr Asn
50 55 60

Ser Asn Asp Ala Ile Glu Asn Arg Ser Lys Asp Ile Thr Gln Ser Thr
65 70 75 80

Thr Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr Pro Gln
85 90 95

Asp Asn Thr Gln Leu Lys Glu Glu Val Val Lys Glu Pro Ser Ser Val
100 105 110

Glu Ser Ser Asn Ser Ser Met Asp Thr Ala Gln Gln Pro Ser His Thr
115 120 125

Thr Ile Asn Ser Glu Ala Ser Ile Gln Thr Ser Asp Asn Glu Glu Asn
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130

135

140

Ser Arg Val Ser Asp Phe Ala Asn Ser Lys Ile Ile Glu Ser Asn Thr
145 150 155 160

Glu Ser Asn Lys Glu Glu Asn Thr Ile Glu Gln Pro Asn Lys Val Arg
165 170 175

Glu Asp Ser Ile Thr Ser Gln Pro Ser Ser Tyr Lys Asn Ile Asp Glu
180 185 190

Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn Glu Tyr
195 200 205

Glu Asn Lys Val Arg Pro Leu Ser Thr Thr Ser Ala Gln Pro Ser Ser
210 215 220

Lys Arg Val Thr Val Asn Gln Leu Ala Ala Glu Gln Gly Ser Asn Val
225 230 235 240

Asn His Leu Ile Lys Val Thr Asp Gln Ser Ile Thr Glu Gly Tyr Asp
245 250 255

Asp Ser Asp Gly Ile Ile Lys Ala His Asp Ala Glu Asn Leu Ile Tyr
260 265 270

Asp Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp Thr Met
275 280 285

Thr Val Asn Ile Asp Lys Asn Thr Val Pro Ser Asp Leu Thr Asp Ser
290 295 300

Phe Ala Ile Pro Lys Ile Lys Asp Asn Ser Gly Glu Ile Ile Ala Thr
305 310 315 320

Gly Thr Tyr Asp Asn Thr Asn Lys Gln Ile Thr Tyr Thr Phe Thr Asp
325 330 335

Tyr Val Asp Lys Tyr Glu Asn Ile Lys Ala His Leu Lys Leu Thr Ser
Page 77

340

345

350

Tyr Ile Asp Lys Ser Lys Val Pro Asn Asn Asn Thr Lys Leu Asp Val
 355 360 365

Glu Tyr Lys Thr Ala Leu Ser Ser Val Asn Lys Thr Ile Thr Val Glu
 370 375 380

Tyr Gln Lys Pro Asn Glu Asn Arg Thr Ala Asn Leu Gln Ser Met Phe
 385 390 395 400

Thr Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile Tyr Ile
 405 410 415

Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile Ser Gly
 420 425 430

Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile Ile Lys
 435 440 445

Val Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn Arg Ile
 450 455 460

Tyr Asp Tyr Ser Glu Tyr Glu Asp Val Thr Asn Asp Asp Tyr Ala Gln
 465 470 475 480

Leu Gly Asn Asn Asn Asp Val Asn Ile Asn Phe Gly Asn Ile Asp Ser
 485 490 495

Pro Tyr Ile Ile Lys Val Ile Ser Lys Tyr Asp Pro Asn Lys Asp Asp
 500 505 510

Tyr Thr Thr Ile Gln Gln Thr Val Thr Met Gln Thr Thr Ile Asn Glu
 515 520 525

Tyr Thr Gly Glu Phe Arg Thr Ala Ser Tyr Asp Asn Thr Ile Ala Phe
 530 535 540

Ser Thr Ser Ser Gly Gln Gly Gln Gly Asp Leu Pro Pro Glu Lys Thr
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545 550 555 560
 Tyr Lys Ile Gly Asp Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Ile
 565 570 575
 Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu Ser Asn Val Leu Val Thr
 580 585 590
 Leu Thr Tyr Pro Asp Gly Thr Ser Lys Ser Val Arg Thr Asp Glu Glu
 595 600 605
 Gly Lys Tyr Gln Phe Asp Gly Leu Lys Asn Gly Leu Thr Tyr Lys Ile
 610 615 620
 Thr Phe Glu Thr Pro Glu Gly Tyr Thr Pro Thr Leu Lys His Ser Gly
 625 630 635 640
 Thr Asn Pro Ala Leu Asp Ser Glu Gly Asn Ser Val Trp Val Thr Ile
 645 650 655
 Asn Gly Gln Asp Asp Met Thr Ile Asp Ser Gly Phe Tyr Gln Thr Pro
 660 665 670
 Lys Tyr Ser Leu Gly Asn Tyr Val Trp Tyr Asp Thr Asn Lys Asp Gly
 675 680 685
 Ile Gln Gly Asp Asp Glu Lys Gly Ile Ser Gly Val Lys Val Thr Leu
 690 695 700
 Lys Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Thr Thr Asp Glu Asn
 705 710 715 720
 Gly Lys Tyr Gln Phe Asp Asn Leu Asn Ser Gly Asn Tyr Ile Val His
 725 730 735
 Phe Asp Lys Pro Ser Gly Met Thr Gln Thr Thr Thr Asp Ser Gly Asp
 740 745 750
 Asp Asp Glu Gln Asp Ala Asp Gly Glu Glu Val His Val Thr Ile Thr
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755

760

765

Asp His Asp Asp Phe Ser Ile Asp Asn Gly Tyr Tyr Asp Asp Asp Ser
770 775 780

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Asp Ser Asp Ser Asp
785 790 795 800

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
805 810 815

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
820 825 830

Ser Asp Ser Asp Ser Asp Ser Gly Leu Asp Asn Ser Ser Asp Lys Asn
835 840 845

Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp His Asp Ser
850 855 860

Lys Gly Thr Leu Leu Gly Ala Leu Phe Ala Gly Leu Gly Ala Leu Leu
865 870 875 880

Leu Gly Lys Arg Arg Lys Asn Arg Lys Asn Lys Asn
885 890

<210> 22
<211> 1973
<212> PRT
<213> Staphylococcus epidermidis

<400> 22

Met Lys Glu Asn Lys Arg Lys Asn Asn Leu Asp Lys Asn Asn Thr Arg
1 5 10 15

Phe Ser Ile Arg Lys Tyr Gln Gly Tyr Gly Ala Thr Ser Val Ala Ile
20 25 30

Ile Gly Phe Ile Ile Ile Ser Cys Phe Ser Glu Ala Lys Ala Asp Ser
35 40 45

P07741US01_6-19-06_Sequence.txt

Asp Lys His Glu Ile Lys Ser His Gln Gln Ser Met Thr Asn His Leu
50 55 60

Thr Thr Leu Pro Ser Asp Asn Gln Glu Asn Thr Ser Asn Asn Glu Phe
65 70 75 80

Asn Asn Arg Asn His Asp Ile Ser His Leu Ser Leu Asn Lys Ser Ile
85 90 95

Gln Met Asp Glu Leu Lys Lys Leu Ile Lys Gln Tyr Lys Ala Ile Asn
100 105 110

Leu Asn Asp Lys Thr Glu Glu Ser Ile Lys Leu Phe Gln Ser Asp Leu
115 120 125

Val Gln Ala Glu Ser Leu Ile Asn Asn Pro Gln Ser Gln Gln His Val
130 135 140

Asp Ala Phe Tyr His Lys Phe Leu Asn Ser Ala Gly Lys Leu Arg Lys
145 150 155 160

Lys Glu Thr Val Ser Ile Lys His Glu Arg Ser Glu Ser Asn Thr Tyr
165 170 175

Arg Leu Gly Asp Glu Val Arg Ser Gln Thr Phe Ser His Ile Arg His
180 185 190

Lys Arg Asn Ala Val Ser Phe Arg Asn Ala Asp Gln Ser Asn Leu Ser
195 200 205

Thr Asp Pro Leu Lys Ala Asn Glu Ile Asn Pro Glu Ile Gln Asn Gly
210 215 220

Asn Phe Ser Gln Val Ser Gly Gly Pro Leu Pro Thr Ser Ser Lys Arg
225 230 235 240

Leu Thr Val Val Thr Asn Val Asp Asn Trp His Ser Tyr Ser Thr Asp
245 250 255

P07741US01_6-19-06_Sequence.txt

Pro Asn Pro Glu Tyr Pro Met Phe Tyr Thr Thr Thr Ala Val Asn Tyr
260 265 270

Pro Asn Phe Met Ser Asn Gly Asn Ala Pro Tyr Gly Val Ile Leu Gly
275 280 285

Arg Thr Thr Asp Gly Trp Asn Arg Asn Val Ile Asp Ser Lys Val Ala
290 295 300

Gly Ile Tyr Gln Asp Ile Asp Val Val Pro Gly Ser Glu Leu Asn Val
305 310 315 320

Asn Phe Ile Ser Thr Ser Pro Val Phe Ser Asp Gly Ala Ala Gly Ala
325 330 335

Lys Leu Lys Ile Ser Asn Val Glu Gln Asn Arg Val Leu Phe Asp Ser
340 345 350

Arg Leu Asn Gly Met Gly Pro Tyr Pro Thr Gly Lys Leu Ser Ala Met
355 360 365

Val Asn Ile Pro Asn Asp Ile Asn Arg Val Arg Ile Ser Phe Leu Pro
370 375 380

Val Ser Ser Thr Gly Arg Val Ser Val Gln Arg Ser Ser Arg Glu His
385 390 395 400

Gly Phe Gly Asp Asn Ser Ser Tyr Tyr His Gly Gly Ser Val Ser Asp
405 410 415

Val Arg Ile Asn Ser Gly Ser Tyr Val Val Ser Lys Val Thr Gln Arg
420 425 430

Glu Tyr Thr Thr Arg Pro Asn Ser Ser Asn Asp Thr Phe Ala Arg Ala
435 440 445

Thr Ile Asn Leu Ser Val Glu Asn Lys Gly His Asn Gln Ser Lys Asp
450 455 460

P07741US01_6-19-06_Sequence.txt

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Thr Tyr Tyr Glu Val Ile Leu Pro Gln Asn Ser Arg Leu Ile Ser Thr
465                               470                     475                   480

Arg Gly Gly Ser Gly Asn Tyr Asn Asn Ala Thr Asn Lys Leu Ser Ile
                               485                     490                   495

Arg Leu Asp Asn Leu Asn Pro Gly Asp Arg Arg Asp Ile Ser Tyr Thr
                               500                     505                   510

Val Asp Phe Glu Ser Ser Ser Pro Lys Leu Ile Asn Leu Asn Ala His
                               515                     520                   525

Leu Leu Tyr Lys Thr Asn Ala Thr Phe Arg Gly Asn Asp Gly Gln Arg
530                               535                     540

Thr Gly Asp Asn Ile Val Asp Leu Gln Ser Ile Ala Leu Leu Met Asn
545                               550                     555                   560

Lys Asp Val Leu Glu Thr Glu Leu Asn Glu Ile Asp Lys Phe Ile Arg
                               565                     570                   575

Asp Leu Asn Glu Ala Asp Phe Thr Ile Asp Ser Trp Ser Ala Leu Gln
                               580                     585                   590

Glu Lys Met Thr Glu Gly Gly Asn Ile Leu Asn Glu Gln Gln Asn Gln
595                               600                     605

Val Ala Leu Glu Asn Gln Ala Ser Gln Glu Thr Ile Asn Asn Val Thr
610                               615                     620

Gln Ser Leu Glu Ile Leu Lys Asn Asn Leu Lys Tyr Lys Thr Pro Ser
625                               630                     635                   640

Gln Pro Ile Ile Lys Ser Asn Asn Gln Ile Pro Asn Ile Thr Ile Ser
645                               650                     655

Pro Ala Asp Lys Ala Asp Lys Leu Thr Ile Thr Tyr Gln Asn Thr Asp
660                               665                     670

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P07741US01_6-19-06_Sequence.txt

Asn Glu Ser Ala Ser Ile Ile Gly Asn Lys Leu Asn Asn Gln Trp Ser
 675 680 685
 Leu Asn Asn Asn Ile Pro Gly Ile Glu Ile Asp Met Gln Thr Gly Leu
 690 695 700
 Val Thr Ile Asp Tyr Lys Ala Val Tyr Pro Glu Ser Val Val Gly Ala
 705 710 715 720
 Asn Asp Lys Thr Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr
 725 730 735
 Met Pro Arg Lys Glu Ala Thr Pro Leu Ser Pro Ile Val Glu Ala Asn
 740 745 750
 Glu Glu Arg Val Asn Val Val Ile Ala Pro Asn Gly Glu Ala Thr Gln
 755 760 765
 Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr Leu Val
 770 775 780
 Ala Ser Lys Asn Gly Ser Ser Trp Thr Leu Asn Lys Gln Ile Asp Tyr
 785 790 795 800
 Val Asn Ile Glu Glu Asn Ser Gly Lys Val Thr Ile Gly Tyr Gln Ala
 805 810
 Val Gln Pro Glu Ser Glu Val Ile Ala Thr Glu Thr Lys Gly Asn Ser
 820 825 830
 Asp Glu Ser Ala Glu Ser Arg Val Thr Met Pro Arg Lys Glu Ala Thr
 835 840 845
 Pro His Ser Pro Ile Val Glu Ala Asn Glu Glu His Val Asn Val Thr
 850 855 860
 Ile Ala Pro Asn Gly Glu Ala Thr Gln Ile Ala Ile Lys Tyr Arg Thr
 865 870 875 880

P07741US01_6-19-06_sequence.txt

Pro Asp Gly Gln Glu Thr Thr Leu Ile Ala Ser Lys Asn Gly Ser Ser
885 890 895

Trp Thr Leu Asn Lys Gln Ile Asp Tyr Val Asn Ile Glu Glu Asn Ser
900 905 910

Gly Lys Val Thr Ile Gly Tyr Gln Ala Val Gln Leu Glu Ser Glu Val
915 920 925

Ile Ala Thr Glu Thr Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg
930 935 940

Ile Thr Met Leu Arg Lys Glu Ala Thr Pro His Ser Pro Ile Val Glu
945 950 955 960

Ala Asn Glu Glu His Val Asn Val Thr Ile Ala Pro Asn Gly Glu Ala
965 970 975

Thr Gln Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr
980 985 990

Leu Val Ala Ser Lys Asn Glu Ser Ser Trp Thr Leu Asn Lys Gln Ile
995 1000 1005

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly
1010 1015 1020

Tyr Gln Ala Val Gln Pro Glu Ser Glu Ile Ile Ala Thr Glu Thr
1025 1030 1035

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr Met Pro
1040 1045 1050

Arg Lys Glu Ala Thr Pro Ile Pro Pro Thr Leu Glu Ala Ser Val
1055 1060 1065

Gln Glu Ala Ser Val Thr Val Thr Pro Asn Glu Asn Ala Thr Lys
1070 1075 1080

P07741US01_6-19-06_Sequence.txt

Val	Phe	Ile	Lys	Tyr	Leu	Asp	Ile	Asn	Asp	Glu	Ile	Ser	Thr	Ile
	1085					1090					1095			
Ile	Ala	Ser	Lys	Ile	Asn	Gln	Gln	Trp	Thr	Leu	Asn	Lys	Asp	Asn
	1100					1105					1110			
Phe	Gly	Ile	Lys	Ile	Asn	Pro	Leu	Thr	Gly	Lys	Val	Ile	Ile	Ser
	1115					1120					1125			
Tyr	Val	Ala	Val	Gln	Pro	Glu	Ser	Asp	Val	Ile	Ala	Ile	Glu	Ser
	1130					1135					1140			
Gln	Gly	Asn	Ser	Asp	Leu	Ser	Glu	Glu	Ser	Arg	Ile	Ile	Met	Pro
	1145					1150					1155			
Thr	Lys	Glu	Glu	Pro	Pro	Glu	Pro	Pro	Ile	Leu	Glu	Ser	Asp	Ser
	1160					1165					1170			
Ile	Glu	Ala	Lys	Val	Asn	Ile	Phe	Pro	Asn	Asp	Glu	Ala	Thr	Arg
	1175					1180					1185			
Ile	Val	Ile	Met	Tyr	Thr	Ser	Leu	Glu	Gly	Gln	Glu	Ala	Thr	Leu
	1190					1195					1200			
Val	Ala	Ser	Lys	Asn	Glu	Ser	Ser	Trp	Thr	Leu	Asn	Lys	Gln	Ile
	1205					1210					1215			
Asp	His	Val	Asn	Ile	Asp	Glu	Asn	Ser	Gly	Lys	Val	Thr	Ile	Gly
	1220					1225					1230			
Tyr	Gln	Ala	Val	Gln	Pro	Glu	Ser	Glu	Val	Ile	Ala	Thr	Glu	Thr
	1235					1240					1245			
Lys	Gly	Asn	Ser	Asp	Ala	Ser	Ala	Glu	Ser	Arg	Val	Thr	Met	Pro
	1250					1255					1260			
Arg	Lys	Glu	Ala	Thr	Pro	His	Ser	Pro	Ile	Val	Glu	Thr	Asn	Glu
	1265					1270					1275			

P07741US01_6-19-06_Sequence.txt

Glu	Arg	Val	Asn	Val	Val	Ile	Ala	Pro	Asn	Gly	Glu	Ala	Thr	Gln
1280						1285					1290			
Ile	Ala	Ile	Lys	Tyr	Arg	Thr	Pro	Asp	Gly	Gln	Glu	Thr	Thr	Leu
1295						1300					1305			
Ile	Ala	Ser	Lys	Asn	Gly	Ser	Ser	Trp	Thr	Leu	Asn	Lys	Gln	Ile
1310						1315					1320			
Asp	His	Val	Asn	Ile	Asp	Glu	Asn	Ser	Gly	Lys	Val	Thr	Ile	Gly
1325						1330					1335			
Tyr	Gln	Ala	Val	Gln	Pro	Glu	Ser	Glu	Ile	Ile	Ala	Thr	Glu	Thr
1340						1345					1350			
Lys	Gly	Asn	Ser	Asp	Ala	Ser	Ala	Glu	Ser	Arg	Ile	Thr	Met	Pro
1355						1360					1365			
Arg	Lys	Glu	Ala	Ile	Pro	His	Ser	Pro	Ile	Val	Glu	Ala	Asn	Glu
1370						1375					1380			
Glu	His	Val	Asn	Val	Thr	Ile	Ala	Pro	Asn	Gly	Glu	Thr	Thr	Gln
1385						1390					1395			
Ile	Ala	Val	Lys	Tyr	Arg	Thr	Pro	Asp	Gly	Gln	Glu	Ala	Thr	Leu
1400						1405					1410			
Ile	Ala	Ser	Lys	Asn	Glu	Ser	Ser	Trp	Thr	Leu	Asn	Lys	Gln	Ile
1415						1420					1425			
Asp	His	Val	Asn	Ile	Asp	Glu	Asn	Ser	Gly	Lys	Val	Thr	Ile	Gly
1430						1435					1440			
Tyr	Gln	Ala	Val	Gln	Pro	Glu	Ser	Glu	Val	Ile	Ala	Thr	Glu	Thr
1445						1450					1455			
Lys	Gly	Asn	Ser	Asp	Ala	Ser	Ala	Glu	Ser	Arg	Ile	Thr	Met	Pro
1460						1465					1470			

P07741US01_6-19-06_Sequence.txt

Val	Lys	Glu	Lys	Thr	Pro	Ala	Pro	Pro	Ile	Ser	Ile	Ile	Asn	Glu
	1475					1480					1485			
Ser	Asn	Ala	Ser	Val	Glu	Ile	Ile	Pro	Gln	Val	Asn	Val	Thr	Gln
	1490					1495					1500			
Leu	Ser	Leu	Gln	Tyr	Ile	Asp	Ala	Lys	Gly	Gln	Gln	Gln	Asn	Leu
	1505					1510					1515			
Ile	Ala	Thr	Leu	Asn	Gln	Asn	Gln	Trp	Thr	Leu	Asn	Lys	Asn	Val
	1520					1525					1530			
Ser	His	Ile	Thr	Val	Asp	Lys	Asn	Thr	Gly	Lys	Val	Leu	Ile	Asn
	1535					1540					1545			
Tyr	Gln	Ala	Val	Tyr	Pro	Glu	Ser	Glu	Val	Ile	Ala	Arg	Glu	Ser
	1550					1555					1560			
Lys	Gly	Asn	Ser	Asp	Ser	Ser	Asn	Val	Ser	Met	Val	Ile	Met	Pro
	1565					1570					1575			
Arg	Lys	Thr	Ala	Thr	Pro	Lys	Pro	Pro	Ile	Ile	Lys	Val	Asp	Glu
	1580					1585					1590			
Met	Asn	Ala	Ser	Leu	Ala	Ile	Ile	Pro	Tyr	Lys	Asn	Asn	Thr	Ala
	1595					1600					1605			
Ile	Asn	Ile	His	Tyr	Ile	Asp	Lys	Lys	Gly	Ile	Lys	Ser	Met	Val
	1610					1615					1620			
Thr	Ala	Ile	Lys	Asn	Asn	Asp	Gln	Trp	Gln	Leu	Asp	Glu	Lys	Ile
	1625					1630					1635			
Lys	Tyr	Val	Lys	Ile	Asp	Ala	Lys	Thr	Gly	Thr	Val	Ile	Ile	Asn
	1640					1645					1650			
Tyr	Gln	Ile	Val	Gln	Glu	Asn	Ser	Glu	Ile	Ile	Ala	Thr	Ala	Ile
	1655					1660					1665			

P07741US01_6-19-06_Sequence.txt

Asn	Gly	Asn	Ser	Asp	Lys	Ser	Glu	Glu	Val	Lys	Val	Leu	Met	Pro
	1670					1675					1680			
Ile	Lys	Glu	Phe	Thr	Pro	Leu	Ala	Pro	Leu	Leu	Glu	Thr	Asn	Tyr
	1685					1690					1695			
Lys	Lys	Ala	Thr	Val	Ser	Ile	Leu	Pro	Gln	Ser	Asn	Ala	Thr	Lys
	1700					1705					1710			
Leu	Asp	Phe	Lys	Tyr	Arg	Asp	Lys	Lys	Gly	Asp	Ser	Lys	Ile	Ile
	1715					1720					1725			
Ile	Val	Lys	Arg	Phe	Lys	Asn	Ile	Trp	Lys	Ala	Asn	Glu	Gln	Ile
	1730					1735					1740			
Ser	Gly	Val	Thr	Ile	Asn	Pro	Glu	Phe	Gly	Gln	Val	Val	Ile	Asn
	1745					1750					1755			
Tyr	Gln	Ala	Val	Tyr	Pro	Glu	Ser	Asp	Ile	Leu	Ala	Ala	Gln	Tyr
	1760					1765					1770			
Val	Gly	Asn	Ser	Asp	Ala	Ser	Glu	Trp	Ala	Lys	Val	Lys	Met	Pro
	1775					1780					1785			
Lys	Lys	Glu	Leu	Ala	Pro	His	Ser	Pro	Ser	Leu	Ile	Tyr	Asp	Asn
	1790					1795					1800			
Arg	Asn	Asn	Lys	Ile	Leu	Ile	Ala	Pro	Asn	Ser	Asn	Ala	Thr	Glu
	1805					1810					1815			
Met	Glu	Leu	Ser	Tyr	Val	Asp	Lys	Asn	Asn	Gln	Ser	Leu	Lys	Val
	1820					1825					1830			
Lys	Ala	Leu	Lys	Ile	Asn	Asn	Arg	Trp	Lys	Phe	Asp	Ser	Ser	Val
	1835					1840					1845			
Ser	Asn	Ile	Ser	Ile	Asn	Pro	Asn	Thr	Gly	Lys	Ile	Val	Leu	Gln
	1850					1855					1860			

P07741US01_6-19-06_Sequence.txt

Pro Gln Phe Leu Leu Thr Asn Ser Lys Ile Ile Val Phe Ala Lys
1865 1870 1875

Lys Gly Asn Ser Asp Ala Ser Ile Ser Val Ser Leu Arg Val Pro
1880 1885 1890

Ala Val Lys Lys Ile Glu Leu Glu Pro Met Phe Asn Val Pro Val
1895 1900 1905

Leu Val Ser Leu Asn Lys Lys Arg Ile Gln Phe Asp Asp Cys Ser
1910 1915 1920

Gly Val Lys Asn Cys Leu Asn Lys Gln Ile Ser Lys Thr Gln Leu
1925 1930 1935

Pro Asp Thr Gly Tyr Ser Asp Lys Ala Ser Lys Ser Asn Ile Leu
1940 1945 1950

Ser Val Leu Leu Leu Gly Phe Gly Phe Leu Ser Tyr Ser Arg Lys
1955 1960 1965

Arg Lys Glu Lys Gln
1970

<210> 23

<211> 10203

<212> PRT

<213> Staphylococcus epidermidis

<400> 23

Met Lys Ser Lys Pro Lys Leu Asn Gly Arg Asn Ile Cys Ser Phe Leu
1 5 10 15

Leu Ser Lys Cys Met Ser Tyr Ser Leu Ser Lys Leu Ser Thr Leu Lys
20 25 30

Thr Tyr Asn Phe Gln Ile Thr Ser Asn Asn Lys Glu Lys Thr Ser Arg
35 40 45

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Ile Gly Val Ala Ile Ala Leu Asn Asn Arg Asp Lys Leu Gln Lys Phe
50 55 60

Ser Ile Arg Lys Tyr Ala Ile Gly Thr Phe Ser Thr Val Ile Ala Thr
65 70 75 80

Leu Val Phe Met Gly Ile Asn Thr Asn His Ala Ser Ala Asp Glu Leu
85 90 95

Asn Gln Asn Gln Lys Leu Ile Lys Gln Leu Asn Gln Thr Asp Asp Asp
100 105 110

Asp Ser Asn Thr His Ser Gln Glu Ile Glu Asn Asn Lys Gln Asn Ser
115 120 125

Ser Gly Lys Thr Glu Ser Leu Arg Ser Ser Thr Ser Gln Asn Gln Ala
130 135 140

Asn Ala Arg Leu Ser Asp Gln Phe Lys Asp Thr Asn Glu Thr Ser Gln
145 150 155 160

Gln Leu Pro Thr Asn Val Ser Asp Asp Ser Ile Asn Gln Ser His Ser
165 170 175

Glu Ala Asn Met Asn Asn Glu Pro Leu Lys Val Asp Asn Ser Thr Met
180 185 190

Gln Ala His Ser Lys Ile Val Ser Asp Ser Asp Gly Asn Ala Ser Glu
195 200 205

Asn Lys His His Lys Leu Thr Glu Asn Val Leu Ala Glu Ser Arg Ala
210 215 220

Ser Lys Asn Asp Lys Glu Lys Glu Asn Leu Gln Glu Lys Asp Lys Ser
225 230 235 240

Gln Gln Val His Pro Pro Leu Asp Lys Asn Ala Leu Gln Ala Phe Phe
245 250 255

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Asp Ala Ser Tyr His Asn Tyr Arg Met Ile Asp Arg Asp Arg Ala Asp
260 265 270

Ala Thr Glu Tyr Gln Lys Val Lys Ser Thr Phe Asp Tyr Val Asn Asp
275 280 285

Leu Leu Gly Asn Asn Gln Asn Ile Pro Ser Glu Gln Leu Val Ser Ala
290 295 300

Tyr Gln Gln Leu Glu Lys Ala Leu Glu Leu Ala Arg Thr Leu Pro Gln
305 310 315 320

Gln Ser Thr Thr Glu Lys Arg Gly Arg Arg Ser Thr Arg Ser Val Val
325 330 335

Glu Asn Arg Ser Ser Arg Ser Asp Tyr Leu Asp Ala Arg Thr Glu Tyr
340 345 350

Tyr Val Ser Lys Asp Asp Asp Asp Ser Gly Phe Pro Pro Gly Thr Phe
355 360 365

Phe His Ala Ser Asn Arg Arg Trp Pro Tyr Asn Leu Pro Arg Ser Arg
370 375 380

Asn Ile Leu Arg Ala Ser Asp Val Gln Gly Asn Ala Tyr Ile Thr Thr
385 390 395 400

Lys Arg Leu Lys Asp Gly Tyr Gln Trp Asp Ile Leu Phe Asn Ser Asn
405 410 415

His Lys Gly His Glu Tyr Met Tyr Tyr Trp Phe Gly Leu Pro Ser Asp
420 425 430

Gln Thr Pro Thr Gly Pro Val Thr Phe Thr Ile Ile Asn Arg Asp Gly
435 440 445

Ser Ser Thr Ser Thr Gly Gly Val Gly Phe Gly Ser Gly Ala Pro Leu
450 455 460

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Pro Gln Phe Trp Arg Ser Ala Gly Ala Ile Asn Ser Ser Val Ala Asn
465 470 475 480

Asp Phe Lys His Gly Ser Ala Thr Asn Tyr Ala Phe Tyr Asp Gly Val
485 490 495

Asn Asn Phe Ser Asp Phe Ala Arg Gly Gly Glu Leu Tyr Phe Asp Arg
500 505 510

Glu Gly Ala Thr Gln Thr Asn Lys Tyr Tyr Gly Asp Glu Asn Phe Ala
515 520 525

Leu Leu Asn Ser Glu Lys Pro Asp Gln Ile Arg Gly Leu Asp Thr Ile
530 535 540

Tyr Ser Phe Lys Gly Ser Gly Asp Val Ser Tyr Arg Ile Ser Phe Lys
545 550 555 560

Thr Gln Gly Ala Pro Thr Ala Arg Leu Tyr Tyr Ala Ala Gly Ala Arg
565 570 575

Ser Gly Glu Tyr Lys Gln Ala Thr Asn Tyr Asn Gln Leu Tyr Val Glu
580 585 590

Pro Tyr Lys Asn Tyr Arg Asn Arg Val Gln Ser Asn Val Gln Val Lys
595 600 605

Asn Arg Thr Leu His Leu Lys Arg Thr Ile Arg Gln Phe Asp Pro Thr
610 615 620

Leu Gln Arg Thr Thr Asp Val Pro Ile Leu Asp Ser Asp Gly Ser Gly
625 630 635 640

Ser Ile Asp Ser Val Tyr Asp Pro Leu Ser Tyr Val Lys Asn Val Thr
645 650 655

Gly Thr Val Leu Gly Ile Tyr Pro Ser Tyr Leu Pro Tyr Asn Gln Glu
660 665 670

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Arg Trp Gln Gly Ala Asn Ala Met Asn Ala Tyr Gln Ile Glu Glu Leu
675 680 685

Phe Ser Gln Glu Asn Leu Gln Asn Ala Ala Arg Ser Gly Arg Pro Ile
690 695 700

Gln Phe Leu Val Gly Phe Asp Val Glu Asp Ser His His Asn Pro Glu
705 710 715 720

Thr Leu Leu Pro Val Asn Leu Tyr Val Lys Pro Glu Leu Lys His Thr
725 730 735

Ile Glu Leu Tyr His Asp Asn Glu Lys Gln Asn Arg Lys Glu Phe Ser
740 745 750

Val Ser Lys Arg Ala Gly His Gly Val Phe Gln Ile Met Ser Gly Thr
755 760 765

Leu His Asn Thr Val Gly Ser Gly Ile Leu Pro Tyr Gln Gln Glu Ile
770 775 780

Arg Ile Lys Leu Thr Ser Asn Glu Pro Ile Lys Asp Ser Glu Trp Ser
785 790 795 800

Ile Thr Gly Tyr Pro Asn Thr Leu Thr Leu Gln Asn Ala Val Gly Arg
805 810 815

Thr Asn Asn Ala Thr Glu Lys Asn Leu Ala Leu Val Gly His Ile Asp
820 825 830

Pro Gly Asn Tyr Phe Ile Thr Val Lys Phe Gly Asp Lys Val Glu Gln
835 840 845

Phe Glu Ile Arg Ser Lys Pro Thr Pro Pro Arg Ile Ile Thr Thr Ala
850 855 860

Asn Glu Leu Arg Gly Asn Ser Asn His Lys Pro Glu Ile Arg Val Thr
865 870 875 880

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Asp Ile Pro Asn Asp Thr Thr Ala Lys Ile Lys Leu Val Met Gly Gly
 885 890 895
 Thr Asp Gly Asp His Asp Pro Glu Ile Asn Pro Tyr Thr Val Pro Glu
 900 905 910
 Asn Tyr Thr Val Val Ala Glu Ala Tyr His Asp Asn Asp Pro Ser Lys
 915 920 925
 Asn Gly Val Leu Thr Phe Arg Ser Ser Asp Tyr Leu Lys Asp Leu Pro
 930 935 940
 Leu Ser Gly Glu Leu Lys Ala Ile Val Tyr Tyr Asn Gln Tyr Val Gln
 945 950 955 960
 Ser Asn Phe Ser Asn Ser Val Pro Phe Ser Ser Asp Thr Thr Pro Pro
 965 970 975
 Thr Ile Asn Glu Pro Ala Gly Leu Val His Lys Tyr Tyr Arg Gly Asp
 980 985 990
 His Val Glu Ile Thr Leu Pro Val Thr Asp Asn Thr Gly Gly Ser Gly
 995 1000 1005
 Leu Arg Asp Val Asn Val Asn Leu Pro Gln Gly Trp Thr Lys Thr
 1010 1015 1020
 Phe Thr Ile Asn Pro Asn Asn Asn Thr Glu Gly Thr Leu Lys Leu
 1025 1030 1035
 Ile Gly Asn Ile Pro Ser Asn Glu Ala Tyr Asn Thr Thr Tyr His
 1040 1045 1050
 Phe Asn Ile Thr Ala Thr Asp Asn Ser Gly Asn Thr Thr Asn Pro
 1055 1060 1065
 Ala Lys Thr Phe Ile Leu Asn Val Gly Lys Leu Ala Asp Asp Leu
 1070 1075 1080

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Asn	Pro	Val	Gly	Leu	Ser	Arg	Asp	Gln	Leu	Gln	Leu	Val	Thr	Asp
	1085					1090					1095			
Pro	Ser	Ser	Leu	Ser	Asn	Ser	Glu	Arg	Glu	Glu	Val	Lys	Arg	Lys
	1100					1105					1110			
Ile	Ser	Glu	Ala	Asn	Ala	Asn	Ile	Arg	Ser	Tyr	Leu	Leu	Gln	Asn
	1115					1120					1125			
Asn	Pro	Ile	Leu	Ala	Gly	Val	Asn	Gly	Asp	Val	Thr	Phe	Tyr	Tyr
	1130					1135					1140			
Arg	Asp	Gly	Ser	Val	Asp	Val	Ile	Asp	Ala	Glu	Asn	Val	Ile	Thr
	1145					1150					1155			
Tyr	Glu	Pro	Glu	Arg	Lys	Ser	Ile	Phe	Ser	Glu	Asn	Gly	Asn	Thr
	1160					1165					1170			
Asn	Lys	Lys	Glu	Ala	Val	Ile	Thr	Ile	Ala	Arg	Gly	Gln	Asn	Tyr
	1175					1180					1185			
Thr	Ile	Gly	Pro	Asn	Leu	Arg	Lys	Tyr	Phe	Ser	Leu	Ser	Asn	Gly
	1190					1195					1200			
Ser	Asp	Leu	Pro	Asn	Arg	Asp	Phe	Thr	Ser	Ile	Ser	Ala	Ile	Gly
	1205					1210					1215			
Ser	Leu	Pro	Ser	Ser	Ser	Glu	Ile	Ser	Arg	Leu	Asn	Val	Gly	Asn
	1220					1225					1230			
Tyr	Asn	Tyr	Arg	Val	Asn	Ala	Lys	Asn	Ala	Tyr	His	Lys	Thr	Gln
	1235					1240					1245			
Gln	Glu	Leu	Asn	Leu	Lys	Leu	Lys	Ile	Val	Glu	Val	Asn	Ala	Pro
	1250					1255					1260			
Thr	Gly	Asn	Asn	Arg	Val	Tyr	Arg	Val	Ser	Thr	Tyr	Asn	Leu	Thr
	1265					1270					1275			

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Asn	Asp	Glu	Ile	Asn	Lys	Ile	Lys	Gln	Ala	Phe	Lys	Ala	Ala	Asn
	1280					1285					1290			
Ser	Gly	Leu	Asn	Leu	Asn	Asp	Asn	Asp	Ile	Thr	Val	Ser	Asn	Asn
	1295					1300					1305			
Phe	Asp	His	Arg	Asn	Val	Ser	Ser	Val	Thr	Val	Thr	Ile	Arg	Lys
	1310					1315					1320			
Gly	Asp	Leu	Ile	Lys	Glu	Phe	Ser	Ser	Asn	Leu	Asn	Asn	Met	Asn
	1325					1330					1335			
Phe	Leu	Arg	Trp	Val	Asn	Ile	Arg	Asp	Asp	Tyr	Thr	Ile	Ser	Trp
	1340					1345					1350			
Thr	Ser	Ser	Lys	Ile	Gln	Gly	Arg	Asn	Thr	Asp	Gly	Gly	Leu	Glu
	1355					1360					1365			
Trp	Ser	Pro	Asp	His	Lys	Ser	Leu	Ile	Tyr	Lys	Tyr	Asp	Ala	Thr
	1370					1375					1380			
Leu	Gly	Arg	Gln	Ile	Asn	Thr	Asn	Asp	Val	Leu	Thr	Leu	Leu	Gln
	1385					1390					1395			
Ala	Thr	Ala	Lys	Asn	Ser	Asn	Leu	Arg	Ser	Asn	Ile	Asn	Ser	Asn
	1400					1405					1410			
Glu	Lys	Gln	Leu	Ala	Glu	Arg	Gly	Ser	Asn	Gly	Tyr	Ser	Lys	Ser
	1415					1420					1425			
Ile	Ile	Arg	Asp	Asp	Gly	Glu	Lys	Ser	Tyr	Leu	Leu	Asn	Ser	Asn
	1430					1435					1440			
Pro	Ile	Gln	Val	Leu	Asp	Leu	Val	Glu	Pro	Asp	Asn	Gly	Tyr	Gly
	1445					1450					1455			
Gly	Arg	Gln	Val	Ser	His	Ser	Asn	Val	Ile	Tyr	Asn	Glu	Lys	Asn
	1460					1465					1470			

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Ser	Ser	Ile	Val	Asn	Gly	Gln	Val	Pro	Glu	Ala	Asn	Gly	Ala	Ser
	1475					1480					1485			
Ala	Phe	Asn	Ile	Asp	Lys	Val	Val	Lys	Ala	Asn	Ala	Ala	Asn	Asn
	1490					1495					1500			
Gly	Ile	Met	Gly	Val	Ile	Tyr	Lys	Ala	Gln	Leu	Tyr	Leu	Ala	Pro
	1505					1510					1515			
Tyr	Ser	Pro	Lys	Gly	Tyr	Ile	Glu	Lys	Leu	Gly	Gln	Asn	Leu	Ser
	1520					1525					1530			
Asn	Thr	Asn	Asn	Val	Ile	Asn	Val	Tyr	Phe	Val	Pro	Ser	Asp	Lys
	1535					1540					1545			
Val	Asn	Pro	Ser	Ile	Thr	Val	Gly	Asn	Tyr	Asp	His	His	Thr	Val
	1550					1555					1560			
Tyr	Ser	Gly	Glu	Thr	Phe	Lys	Asn	Thr	Ile	Asn	Val	Asn	Asp	Asn
	1565					1570					1575			
Tyr	Gly	Leu	Asn	Thr	Val	Ala	Ser	Thr	Ser	Asp	Ser	Ala	Ile	Thr
	1580					1585					1590			
Met	Thr	Arg	Asn	Asn	Asn	Glu	Leu	Val	Gly	Gln	Ala	Pro	Asn	Val
	1595					1600					1605			
Thr	Asn	Ser	Thr	Asn	Lys	Ile	Val	Lys	Val	Lys	Ala	Thr	Asp	Lys
	1610					1615					1620			
Ser	Gly	Asn	Glu	Ser	Ile	Val	Ser	Phe	Thr	Val	Asn	Ile	Lys	Pro
	1625					1630					1635			
Leu	Asn	Glu	Lys	Tyr	Arg	Ile	Thr	Thr	Ser	Ser	Ser	Asn	Gln	Thr
	1640					1645					1650			
Pro	Val	Arg	Ile	Ser	Asn	Ile	Gln	Asn	Asn	Ala	Asn	Leu	Ser	Ile
	1655					1660					1665			

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Glu	Asp	Gln	Asn	Arg	Val	Lys	Ser	Ser	Leu	Ser	Met	Thr	Lys	Ile
	1670					1675					1680			
Leu	Gly	Thr	Arg	Asn	Tyr	Val	Asn	Glu	Ser	Asn	Asn	Asp	Val	Arg
	1685					1690					1695			
Ser	Gln	Val	Val	Ser	Lys	Val	Asn	Arg	Ser	Gly	Asn	Asn	Ala	Thr
	1700					1705					1710			
Val	Asn	Val	Thr	Thr	Thr	Phe	Ser	Asp	Gly	Thr	Thr	Asn	Thr	Ile
	1715					1720					1725			
Thr	Val	Pro	Val	Lys	His	Val	Leu	Leu	Glu	Val	Val	Pro	Thr	Thr
	1730					1735					1740			
Arg	Thr	Thr	Val	Arg	Gly	Gln	Gln	Phe	Pro	Thr	Gly	Lys	Gly	Thr
	1745					1750					1755			
Ser	Pro	Asn	Asp	Phe	Phe	Ser	Leu	Arg	Thr	Gly	Gly	Pro	Val	Asp
	1760					1765					1770			
Ala	Arg	Ile	Val	Trp	Val	Asn	Asn	Gln	Gly	Pro	Asp	Ile	Asn	Ser
	1775					1780					1785			
Asn	Gln	Ile	Gly	Arg	Asp	Leu	Thr	Leu	His	Ala	Glu	Ile	Phe	Phe
	1790					1795					1800			
Asp	Gly	Glu	Thr	Thr	Pro	Ile	Arg	Lys	Asp	Thr	Thr	Tyr	Lys	Leu
	1805					1810					1815			
Ser	Gln	Ser	Ile	Pro	Lys	Gln	Ile	Tyr	Glu	Thr	Thr	Ile	Asn	Gly
	1820					1825					1830			
Arg	Phe	Asn	Ser	Ser	Gly	Asp	Ala	Tyr	Pro	Gly	Asn	Phe	Val	Gln
	1835					1840					1845			
Ala	Val	Asn	Gln	Tyr	Trp	Pro	Glu	His	Met	Asp	Phe	Arg	Trp	Ala
	1850					1855					1860			

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Gln	Gly	Ser	Gly	Thr	Pro	Ser	Ser	Arg	Asn	Ala	Gly	Ser	Phe	Thr
	1865					1870					1875			
Lys	Thr	Val	Thr	Val	Val	Tyr	Gln	Asn	Gly	Gln	Thr	Glu	Asn	Val
	1880					1885					1890			
Asn	Val	Leu	Phe	Lys	Val	Lys	Pro	Asn	Lys	Pro	Val	Ile	Asp	Ser
	1895					1900					1905			
Asn	Ser	Val	Ile	Ser	Lys	Gly	Gln	Leu	Asn	Gly	Gln	Gln	Ile	Leu
	1910					1915					1920			
Val	Arg	Asn	Val	Pro	Gln	Asn	Ala	Gln	Val	Thr	Leu	Tyr	Gln	Ser
	1925					1930					1935			
Asn	Gly	Thr	Val	Ile	Pro	Asn	Thr	Asn	Thr	Thr	Ile	Asp	Ser	Asn
	1940					1945					1950			
Gly	Ile	Ala	Thr	Val	Thr	Ile	Gln	Gly	Thr	Leu	Pro	Thr	Gly	Asn
	1955					1960					1965			
Ile	Thr	Ala	Lys	Thr	Ser	Met	Thr	Asn	Asn	Val	Thr	Tyr	Thr	Lys
	1970					1975					1980			
Gln	Asn	Ser	Ser	Gly	Ile	Ala	Ser	Asn	Thr	Thr	Glu	Asp	Ile	Ser
	1985					1990					1995			
Val	Phe	Ser	Glu	Asn	Ser	Asp	Gln	Val	Asn	Val	Thr	Ala	Gly	Met
	2000					2005					2010			
Gln	Ala	Lys	Asn	Asp	Gly	Ile	Lys	Ile	Ile	Lys	Gly	Thr	Asn	Tyr
	2015					2020					2025			
Asn	Phe	Asn	Asp	Phe	Asn	Ser	Phe	Ile	Ser	Asn	Ile	Pro	Ala	His
	2030					2035					2040			
Ser	Thr	Leu	Thr	Trp	Asn	Glu	Glu	Pro	Asn	Ser	Trp	Lys	Asn	Asn
	2045					2050					2055			

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Ile	Gly	Thr	Thr	Thr	Lys	Thr	Val	Thr	Val	Thr	Leu	Pro	Asn	His
	2060					2065					2070			
Gln	Gly	Thr	Arg	Thr	Val	Asp	Ile	Pro	Ile	Thr	Ile	Tyr	Pro	Thr
	2075					2080					2085			
Val	Thr	Ala	Lys	Asn	Pro	Val	Arg	Asp	Gln	Lys	Gly	Arg	Asn	Leu
	2090					2095					2100			
Thr	Asn	Gly	Thr	Asp	Val	Tyr	Asn	Tyr	Ile	Ile	Phe	Glu	Asn	Asn
	2105					2110					2115			
Asn	Arg	Leu	Gly	Gly	Thr	Ala	Ser	Trp	Lys	Asp	Asn	Arg	Gln	Pro
	2120					2125					2130			
Asp	Lys	Asn	Ile	Ala	Gly	Val	Gln	Asn	Leu	Ile	Ala	Leu	Val	Asn
	2135					2140					2145			
Tyr	Pro	Gly	Ile	Ser	Thr	Pro	Leu	Glu	Val	Pro	Val	Lys	Val	Trp
	2150					2155					2160			
Val	Tyr	Asn	Phe	Asp	Phe	Thr	Gln	Pro	Ile	Tyr	Lys	Ile	Gln	Val
	2165					2170					2175			
Gly	Asp	Thr	Phe	Pro	Lys	Gly	Thr	Trp	Ala	Gly	Tyr	Tyr	Lys	His
	2180					2185					2190			
Leu	Glu	Asn	Gly	Glu	Gly	Leu	Pro	Ile	Asp	Gly	Trp	Lys	Phe	Tyr
	2195					2200					2205			
Trp	Asn	Gln	Gln	Ser	Thr	Gly	Thr	Thr	Ser	Asp	Gln	Trp	Gln	Ser
	2210					2215					2220			
Leu	Ala	Tyr	Thr	Arg	Thr	Pro	Phe	Val	Lys	Thr	Gly	Thr	Tyr	Asp
	2225					2230					2235			
Val	Val	Asn	Pro	Ser	Asn	Trp	Gly	Val	Trp	Gln	Thr	Ser	Gln	Ser
	2240					2245					2250			

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Ala	Lys	Phe	Ile	Val	Thr	Asn	Ala	Lys	Pro	Asn	Gln	Pro	Thr	Ile
	2255					2260					2265			
Thr	Gln	Ser	Lys	Thr	Gly	Asp	Val	Thr	Val	Thr	Pro	Gly	Ala	Val
	2270					2275					2280			
Arg	Asn	Ile	Leu	Ile	Ser	Gly	Thr	Asn	Asp	Tyr	Ile	Gln	Ala	Ser
	2285					2290					2295			
Ala	Asp	Lys	Ile	Val	Ile	Asn	Lys	Asn	Gly	Asn	Lys	Leu	Thr	Thr
	2300					2305					2310			
Phe	Val	Lys	Asn	Asn	Asp	Gly	Arg	Trp	Thr	Val	Glu	Thr	Gly	Ser
	2315					2320					2325			
Pro	Asp	Ile	Asn	Gly	Ile	Gly	Pro	Thr	Asn	Asn	Gly	Thr	Ala	Ile
	2330					2335					2340			
Ser	Leu	Ser	Arg	Leu	Ala	Val	Arg	Pro	Gly	Asp	Ser	Ile	Glu	Ala
	2345					2350					2355			
Ile	Ala	Thr	Glu	Gly	Ser	Gly	Glu	Thr	Ile	Ser	Thr	Ser	Ala	Thr
	2360					2365					2370			
Ser	Glu	Ile	Tyr	Ile	Val	Lys	Ala	Pro	Gln	Pro	Glu	Gln	Val	Ala
	2375					2380					2385			
Thr	His	Thr	Tyr	Asp	Asn	Gly	Thr	Phe	Asp	Ile	Leu	Pro	Asp	Asn
	2390					2395					2400			
Ser	Arg	Asn	Ser	Leu	Asn	Pro	Thr	Glu	Arg	Val	Glu	Ile	Asn	Tyr
	2405					2410					2415			
Thr	Glu	Lys	Leu	Asn	Gly	Asn	Glu	Thr	Gln	Lys	Ser	Phe	Thr	Ile
	2420					2425					2430			
Thr	Lys	Asn	Asn	Asn	Gly	Lys	Trp	Thr	Ile	Asn	Asn	Lys	Pro	Asn
	2435					2440					2445			

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Tyr	Val	Glu	Phe	Asn	Gln	Asp	Asn	Gly	Lys	Val	Val	Phe	Ser	Ala
	2450					2455					2460			
Asn	Thr	Ile	Lys	Pro	Asn	Ser	Gln	Ile	Thr	Ile	Thr	Pro	Lys	Ala
	2465					2470					2475			
Gly	Gln	Gly	Asn	Thr	Glu	Asn	Thr	Asn	Pro	Thr	Val	Ile	Gln	Ala
	2480					2485					2490			
Pro	Ala	Gln	His	Thr	Leu	Thr	Ile	Asn	Glu	Ile	Val	Lys	Glu	Gln
	2495					2500					2505			
Gly	Gln	Asn	Val	Thr	Asn	Asp	Asp	Ile	Asn	Asn	Ala	Val	Gln	Val
	2510					2515					2520			
Pro	Asn	Lys	Asn	Arg	Val	Ala	Ile	Lys	Gln	Gly	Asn	Ala	Leu	Pro
	2525					2530					2535			
Thr	Asn	Leu	Ala	Gly	Gly	Ser	Thr	Ser	His	Ile	Pro	Val	Val	Ile
	2540					2545					2550			
Tyr	Tyr	Ser	Asp	Gly	Ser	Ser	Glu	Glu	Ala	Thr	Glu	Thr	Val	Arg
	2555					2560					2565			
Thr	Lys	Val	Asn	Lys	Thr	Glu	Leu	Ile	Asn	Ala	Arg	Arg	Arg	Leu
	2570					2575					2580			
Asp	Glu	Glu	Ile	Ser	Lys	Glu	Asn	Lys	Thr	Pro	Ser	Ser	Ile	Arg
	2585					2590					2595			
Asn	Phe	Asp	Gln	Ala	Met	Asn	Arg	Ala	Gln	Ser	Gln	Ile	Asn	Thr
	2600					2605					2610			
Ala	Lys	Ser	Asp	Ala	Asp	Gln	Val	Ile	Gly	Thr	Glu	Phe	Ala	Thr
	2615					2620					2625			
Pro	Gln	Gln	Val	Asn	Ser	Ala	Leu	Ser	Lys	Val	Gln	Ala	Ala	Gln
	2630					2635					2640			

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Asn	Lys	Ile	Asn	Glu	Ala	Lys	Ala	Leu	Leu	Gln	Asn	Lys	Ala	Asp
	2645					2650					2655			
Asn	Ser	Gln	Leu	Val	Arg	Ala	Lys	Glu	Gln	Leu	Gln	Gln	Ser	Ile
	2660					2665					2670			
Gln	Pro	Ala	Ala	Ser	Thr	Asp	Gly	Met	Thr	Gln	Asp	Ser	Thr	Arg
	2675					2680					2685			
Asn	Tyr	Lys	Asn	Lys	Arg	Gln	Ala	Ala	Glu	Gln	Ala	Ile	Gln	His
	2690					2695					2700			
Ala	Asn	Ser	Val	Ile	Asn	Asn	Gly	Asp	Ala	Thr	Ser	Gln	Gln	Ile
	2705					2710					2715			
Asn	Asp	Ala	Lys	Asn	Thr	Val	Glu	Gln	Ala	Gln	Arg	Asp	Tyr	Val
	2720					2725					2730			
Glu	Ala	Lys	Ser	Asn	Leu	Arg	Ala	Asp	Lys	Ser	Gln	Leu	Gln	Ser
	2735					2740					2745			
Ala	Tyr	Asp	Thr	Leu	Asn	Arg	Asp	Val	Leu	Thr	Asn	Asp	Lys	Lys
	2750					2755					2760			
Pro	Ala	Ser	Val	Arg	Arg	Tyr	Asn	Glu	Ala	Ile	Ser	Asn	Ile	Arg
	2765					2770					2775			
Lys	Glu	Leu	Asp	Thr	Ala	Lys	Ala	Asp	Ala	Ser	Ser	Thr	Leu	Arg
	2780					2785					2790			
Asn	Thr	Asn	Pro	Ser	Val	Glu	Gln	Val	Arg	Asp	Ala	Leu	Asn	Lys
	2795					2800					2805			
Ile	Asn	Thr	Val	Gln	Pro	Lys	Val	Asn	Gln	Ala	Ile	Ala	Leu	Leu
	2810					2815					2820			
Gln	Pro	Lys	Glu	Asn	Asn	Ser	Glu	Leu	Val	Gln	Ala	Lys	Lys	Arg
	2825					2830					2835			

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Leu	Gln	Asp	Ala	Val	Asn	Asp	Ile	Pro	Gln	Thr	Gln	Gly	Met	Thr
	2840					2845					2850			
Gln	Gln	Thr	Ile	Asn	Asn	Tyr	Asn	Asp	Lys	Gln	Arg	Glu	Ala	Glu
	2855					2860					2865			
Arg	Ala	Leu	Thr	Ser	Ala	Gln	Arg	Val	Ile	Asp	Asn	Gly	Asp	Ala
	2870					2875					2880			
Thr	Thr	Gln	Glu	Ile	Thr	Ser	Glu	Lys	Ser	Lys	Val	Glu	Gln	Ala
	2885					2890					2895			
Met	Gln	Ala	Leu	Thr	Asn	Ala	Lys	Ser	Asn	Leu	Arg	Ala	Asp	Lys
	2900					2905					2910			
Asn	Glu	Leu	Gln	Thr	Ala	Tyr	Asn	Lys	Leu	Ile	Glu	Asn	Val	Ser
	2915					2920					2925			
Thr	Asn	Gly	Lys	Lys	Pro	Ala	Ser	Ile	Arg	Gln	Tyr	Glu	Thr	Ala
	2930					2935					2940			
Lys	Ala	Arg	Ile	Gln	Asn	Gln	Ile	Asn	Asp	Ala	Lys	Asn	Glu	Ala
	2945					2950					2955			
Glu	Arg	Ile	Leu	Gly	Asn	Asp	Asn	Pro	Gln	Val	Ser	Gln	Val	Thr
	2960					2965					2970			
Gln	Ala	Leu	Asn	Lys	Ile	Lys	Ala	Ile	Gln	Pro	Lys	Leu	Thr	Glu
	2975					2980					2985			
Ala	Ile	Asn	Met	Leu	Gln	Asn	Lys	Glu	Asn	Asn	Thr	Glu	Leu	Val
	2990					2995					3000			
Asn	Ala	Lys	Asn	Arg	Leu	Glu	Asn	Ala	Val	Asn	Asp	Thr	Asp	Pro
	3005					3010					3015			
Thr	His	Gly	Met	Thr	Gln	Glu	Thr	Ile	Asn	Asn	Tyr	Asn	Ala	Lys
	3020					3025					3030			

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Lys Arg Glu Ala Gln Asn Glu Ile Gln Lys Ala Asn Met Ile Ile
 3035 3040 3045
 Asn Asn Gly Asp Ala Thr Ala Gln Asp Ile Ser Ser Glu Lys Ser
 3050 3055 3060
 Lys Val Glu Gln Val Leu Gln Ala Leu Gln Asn Ala Lys Asn Asp
 3065 3070 3075
 Leu Arg Ala Asp Lys Arg Glu Leu Gln Thr Ala Tyr Asn Lys Leu
 3080 3085 3090
 Ile Gln Asn Val Asn Thr Asn Gly Lys Lys Pro Ser Ser Ile Gln
 3095 3100 3105
 Asn Tyr Lys Ser Ala Arg Arg Asn Ile Glu Asn Gln Tyr Asn Thr
 3110 3115 3120
 Ala Lys Asn Glu Ala His Asn Val Leu Glu Asn Thr Asn Pro Thr
 3125 3130 3135
 Val Asn Ala Val Glu Asp Ala Leu Arg Lys Ile Asn Ala Ile Gln
 3140 3145 3150
 Pro Glu Val Thr Lys Ala Ile Asn Ile Leu Gln Asp Lys Glu Asp
 3155 3160 3165
 Asn Ser Glu Leu Val Arg Ala Lys Glu Lys Leu Asp Gln Ala Ile
 3170 3175 3180
 Asn Ser Gln Pro Ser Leu Asn Gly Met Thr Gln Glu Ser Ile Asn
 3185 3190 3195
 Asn Tyr Thr Thr Lys Arg Arg Glu Ala Gln Asn Ile Ala Ser Ser
 3200 3205 3210
 Ala Asp Thr Ile Ile Asn Asn Gly Asp Ala Ser Ile Glu Gln Ile
 3215 3220 3225

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Thr	Glu	Asn	Lys	Ile	Arg	Val	Glu	Glu	Ala	Thr	Asn	Ala	Leu	Asn
	3230					3235					3240			
Glu	Ala	Lys	Gln	His	Leu	Thr	Ala	Asp	Thr	Thr	Ser	Leu	Lys	Thr
	3245					3250					3255			
Glu	Val	Arg	Lys	Leu	Ser	Arg	Arg	Gly	Asp	Thr	Asn	Asn	Lys	Lys
	3260					3265					3270			
Pro	Ser	Ser	Val	Ser	Ala	Tyr	Asn	Asn	Thr	Ile	His	Ser	Leu	Gln
	3275					3280					3285			
Ser	Glu	Ile	Thr	Gln	Thr	Glu	Asn	Arg	Ala	Asn	Thr	Ile	Ile	Asn
	3290					3295					3300			
Lys	Pro	Ile	Arg	Ser	Val	Glu	Glu	Val	Asn	Asn	Ala	Leu	His	Glu
	3305					3310					3315			
Val	Asn	Gln	Leu	Asn	Gln	Arg	Leu	Thr	Asp	Thr	Ile	Asn	Leu	Leu
	3320					3325					3330			
Gln	Pro	Leu	Ala	Asn	Lys	Glu	Ser	Leu	Lys	Glu	Ala	Arg	Asn	Arg
	3335					3340					3345			
Leu	Glu	Ser	Lys	Ile	Asn	Glu	Thr	Val	Gln	Thr	Asp	Gly	Met	Thr
	3350					3355					3360			
Gln	Gln	Ser	Val	Glu	Asn	Tyr	Lys	Gln	Ala	Lys	Ile	Lys	Ala	Gln
	3365					3370					3375			
Asn	Glu	Ser	Ser	Ile	Ala	Gln	Thr	Leu	Ile	Asn	Asn	Gly	Asp	Ala
	3380					3385					3390			
Ser	Asp	Gln	Glu	Val	Ser	Thr	Glu	Ile	Glu	Lys	Leu	Asn	Gln	Lys
	3395					3400					3405			
Leu	Ser	Glu	Leu	Thr	Asn	Ser	Ile	Asn	His	Leu	Thr	Val	Asn	Lys
	3410					3415					3420			

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Glu	Pro	Leu	Glu	Thr	Ala	Lys	Asn	Gln	Leu	Gln	Ala	Asn	Ile	Asp
	3425					3430					3435			
Gln	Lys	Pro	Ser	Thr	Asp	Gly	Met	Thr	Gln	Gln	Ser	Val	Gln	Ser
	3440					3445					3450			
Tyr	Glu	Arg	Lys	Leu	Gln	Glu	Ala	Lys	Asp	Lys	Ile	Asn	Ser	Ile
	3455					3460					3465			
Asn	Asn	Val	Leu	Ala	Asn	Asn	Pro	Asp	Val	Asn	Ala	Ile	Arg	Thr
	3470					3475					3480			
Asn	Lys	Val	Glu	Thr	Glu	Gln	Ile	Asn	Asn	Glu	Leu	Thr	Gln	Ala
	3485					3490					3495			
Lys	Gln	Gly	Leu	Thr	Val	Asp	Lys	Gln	Pro	Leu	Ile	Asn	Ala	Lys
	3500					3505					3510			
Thr	Ala	Leu	Gln	Gln	Ser	Leu	Asp	Asn	Gln	Pro	Ser	Thr	Thr	Gly
	3515					3520					3525			
Met	Thr	Glu	Ala	Thr	Ile	Gln	Asn	Tyr	Asn	Ala	Lys	Arg	Gln	Lys
	3530					3535					3540			
Ala	Glu	Gln	Val	Ile	Gln	Asn	Ala	Asn	Lys	Ile	Ile	Glu	Asn	Ala
	3545					3550					3555			
Gln	Pro	Ser	Val	Gln	Gln	Val	Ser	Asp	Glu	Lys	Ser	Lys	Val	Glu
	3560					3565					3570			
Gln	Ala	Leu	Ser	Glu	Leu	Asn	Asn	Ala	Lys	Ser	Ala	Leu	Arg	Ala
	3575					3580					3585			
Asp	Lys	Gln	Glu	Leu	Gln	Gln	Ala	Tyr	Asn	Gln	Leu	Ile	Gln	Pro
	3590					3595					3600			
Thr	Asp	Leu	Asn	Asn	Lys	Lys	Pro	Ala	Ser	Ile	Thr	Ala	Tyr	Asn
	3605					3610					3615			

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Gln	Arg	Tyr	Gln	Gln	Phe	Ser	Asn	Glu	Leu	Asn	Ser	Thr	Lys	Thr
	3620					3625					3630			
Asn	Thr	Asp	Arg	Ile	Leu	Lys	Glu	Gln	Asn	Pro	Ser	Val	Ala	Asp
	3635					3640					3645			
Val	Asn	Asn	Ala	Leu	Asn	Lys	Val	Arg	Glu	Val	Gln	Gln	Lys	Leu
	3650					3655					3660			
Asn	Glu	Ala	Arg	Ala	Leu	Leu	Gln	Asn	Lys	Glu	Asp	Asn	Ser	Ala
	3665					3670					3675			
Leu	Val	Arg	Ala	Lys	Glu	Gln	Leu	Gln	Gln	Ala	Val	Asp	Gln	Val
	3680					3685					3690			
Pro	Ser	Thr	Glu	Gly	Met	Thr	Gln	Gln	Thr	Lys	Asp	Asp	Tyr	Asn
	3695					3700					3705			
Ser	Lys	Gln	Gln	Ala	Ala	Gln	Gln	Glu	Ile	Ser	Lys	Ala	Gln	Gln
	3710					3715					3720			
Val	Ile	Asp	Asn	Gly	Asp	Ala	Thr	Thr	Gln	Gln	Ile	Ser	Asn	Ala
	3725					3730					3735			
Lys	Thr	Asn	Val	Glu	Arg	Ala	Leu	Glu	Ala	Leu	Asn	Asn	Ala	Lys
	3740					3745					3750			
Thr	Gly	Leu	Arg	Ala	Asp	Lys	Glu	Glu	Leu	Gln	Asn	Ala	Tyr	Asn
	3755					3760					3765			
Gln	Leu	Thr	Gln	Asn	Ile	Asp	Thr	Ser	Gly	Lys	Thr	Pro	Ala	Ser
	3770					3775					3780			
Ile	Arg	Lys	Tyr	Asn	Glu	Ala	Lys	Ser	Arg	Ile	Gln	Thr	Gln	Ile
	3785					3790					3795			
Asp	Ser	Ala	Lys	Asn	Glu	Ala	Asn	Ser	Ile	Leu	Thr	Asn	Asp	Asn
	3800					3805					3810			

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Pro	Gln	Val	Ser	Gln	Val	Thr	Ala	Ala	Leu	Asn	Lys	Ile	Lys	Ala
	3815					3820					3825			
Val	Gln	Pro	Glu	Leu	Asp	Lys	Ala	Ile	Ala	Met	Leu	Lys	Asn	Lys
	3830					3835					3840			
Glu	Asn	Asn	Asn	Ala	Leu	Val	Gln	Ala	Lys	Gln	Gln	Leu	Gln	Gln
	3845					3850					3855			
Ile	Val	Asn	Glu	Val	Asp	Pro	Thr	Gln	Gly	Met	Thr	Thr	Asp	Thr
	3860					3865					3870			
Ala	Asn	Asn	Tyr	Lys	Ser	Lys	Lys	Arg	Glu	Ala	Glu	Asp	Glu	Ile
	3875					3880					3885			
Gln	Lys	Ala	Gln	Gln	Ile	Ile	Asn	Asn	Gly	Asp	Ala	Thr	Glu	Gln
	3890					3895					3900			
Gln	Ile	Thr	Asn	Glu	Thr	Asn	Arg	Val	Asn	Gln	Ala	Ile	Asn	Ala
	3905					3910					3915			
Ile	Asn	Lys	Ala	Lys	Asn	Asp	Leu	Arg	Ala	Asp	Lys	Ser	Gln	Leu
	3920					3925					3930			
Glu	Asn	Ala	Tyr	Asn	Gln	Leu	Ile	Gln	Asn	Val	Asp	Thr	Asn	Gly
	3935					3940					3945			
Lys	Lys	Pro	Ala	Ser	Ile	Gln	Gln	Tyr	Gln	Ala	Ala	Arg	Gln	Ala
	3950					3955					3960			
Ile	Glu	Thr	Gln	Tyr	Asn	Asn	Ala	Lys	Ser	Glu	Ala	His	Gln	Ile
	3965					3970					3975			
Leu	Glu	Asn	Ser	Asn	Pro	Ser	Val	Asn	Glu	Val	Ala	Gln	Ala	Leu
	3980					3985					3990			
Gln	Lys	Val	Glu	Ala	Val	Gln	Leu	Lys	Val	Asn	Asp	Ala	Ile	His
	3995					4000					4005			

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Ile	Leu	Gln	Asn	Lys	Glu	Asn	Asn	Ser	Ala	Leu	Val	Thr	Ala	Lys
	4010					4015					4020			
Asn	Gln	Leu	Gln	Gln	Ser	Val	Asn	Asp	Gln	Pro	Leu	Thr	Thr	Gly
	4025					4030					4035			
Met	Thr	Gln	Asp	Ser	Ile	Asn	Asn	Tyr	Glu	Ala	Lys	Arg	Asn	Glu
	4040					4045					4050			
Ala	Gln	Ser	Ala	Ile	Arg	Asn	Ala	Glu	Ala	Val	Ile	Asn	Asn	Gly
	4055					4060					4065			
Asp	Ala	Thr	Ala	Lys	Gln	Ile	Ser	Asp	Glu	Lys	Ser	Lys	Val	Glu
	4070					4075					4080			
Gln	Ala	Leu	Ala	His	Leu	Asn	Asp	Ala	Lys	Gln	Gln	Leu	Thr	Ala
	4085					4090					4095			
Asp	Thr	Thr	Glu	Leu	Gln	Thr	Ala	Val	Gln	Gln	Leu	Asn	Arg	Arg
	4100					4105					4110			
Gly	Asp	Thr	Asn	Asn	Lys	Lys	Pro	Arg	Ser	Ile	Asn	Ala	Tyr	Asn
	4115					4120					4125			
Lys	Ala	Ile	Gln	Ser	Leu	Glu	Thr	Gln	Ile	Thr	Ser	Ala	Lys	Asp
	4130					4135					4140			
Asn	Ala	Asn	Ala	Val	Ile	Gln	Lys	Pro	Ile	Arg	Thr	Val	Gln	Glu
	4145					4150					4155			
Val	Asn	Asn	Ala	Leu	Gln	Gln	Val	Asn	Gln	Leu	Asn	Gln	Gln	Leu
	4160					4165					4170			
Thr	Glu	Ala	Ile	Asn	Gln	Leu	Gln	Pro	Leu	Ser	Asn	Asn	Asp	Ala
	4175					4180					4185			
Leu	Lys	Ala	Ala	Arg	Leu	Asn	Leu	Glu	Asn	Lys	Ile	Asn	Gln	Thr
	4190					4195					4200			

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Val	Gln	Thr	Asp	Gly	Met	Thr	Gln	Gln	Ser	Ile	Glu	Ala	Tyr	Gln
4205						4210					4215			
Asn	Ala	Lys	Arg	Val	Ala	Gln	Asn	Glu	Ser	Asn	Thr	Ala	Leu	Ala
4220						4225					4230			
Leu	Ile	Asn	Asn	Gly	Asp	Ala	Asp	Glu	Gln	Gln	Ile	Thr	Thr	Glu
4235						4240					4245			
Thr	Asp	Arg	Val	Asn	Gln	Gln	Thr	Thr	Asn	Leu	Thr	Gln	Ala	Ile
4250						4255					4260			
Asn	Gly	Leu	Thr	Val	Asn	Lys	Glu	Pro	Leu	Glu	Thr	Ala	Lys	Thr
4265						4270					4275			
Ala	Leu	Gln	Asn	Asn	Ile	Asp	Gln	Val	Pro	Ser	Thr	Asp	Gly	Met
4280						4285					4290			
Thr	Gln	Gln	Ser	Val	Ala	Asn	Tyr	Asn	Gln	Lys	Leu	Gln	Ile	Ala
4295						4300					4305			
Lys	Asn	Glu	Ile	Asn	Thr	Ile	Asn	Asn	Val	Leu	Ala	Asn	Asn	Pro
4310						4315					4320			
Asp	Val	Asn	Ala	Ile	Lys	Thr	Asn	Lys	Ala	Glu	Ala	Glu	Arg	Ile
4325						4330					4335			
Ser	Asn	Asp	Leu	Thr	Gln	Ala	Lys	Asn	Asn	Leu	Gln	Val	Asp	Thr
4340						4345					4350			
Gln	Pro	Leu	Glu	Lys	Ile	Lys	Arg	Gln	Leu	Gln	Asp	Glu	Ile	Asp
4355						4360					4365			
Gln	Gly	Thr	Asn	Thr	Asp	Gly	Met	Thr	Gln	Asp	Ser	Val	Asp	Asn
4370						4375					4380			
Tyr	Asn	Asp	Ser	Leu	Ser	Ala	Ala	Ile	Ile	Glu	Lys	Gly	Lys	Val
4385						4390					4395			

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Asn	Lys	Leu	Leu	Lys	Arg	Asn	Pro	Thr	Val	Glu	Gln	Val	Lys	Glu
	4400					4405					4410			
Ser	Val	Ala	Asn	Ala	Gln	Gln	Val	Ile	Gln	Asp	Leu	Gln	Asn	Ala
	4415					4420					4425			
Arg	Thr	Ser	Leu	Val	Pro	Asp	Lys	Thr	Gln	Leu	Gln	Glu	Ala	Lys
	4430					4435					4440			
Asn	Arg	Leu	Glu	Asn	Ser	Ile	Asn	Gln	Gln	Thr	Asp	Thr	Asp	Gly
	4445					4450					4455			
Met	Thr	Gln	Asp	Ser	Leu	Asn	Asn	Tyr	Asn	Asp	Lys	Leu	Ala	Lys
	4460					4465					4470			
Ala	Arg	Gln	Asn	Leu	Glu	Lys	Ile	Ser	Lys	Val	Leu	Gly	Gly	Gln
	4475					4480					4485			
Pro	Thr	Val	Ala	Glu	Ile	Arg	Gln	Asn	Thr	Asp	Glu	Ala	Asn	Ala
	4490					4495					4500			
His	Lys	Gln	Ala	Leu	Asp	Thr	Ala	Arg	Ser	Gln	Leu	Thr	Leu	Asn
	4505					4510					4515			
Arg	Glu	Pro	Tyr	Ile	Asn	His	Ile	Asn	Asn	Glu	Ser	His	Leu	Asn
	4520					4525					4530			
Asn	Ala	Gln	Lys	Asp	Asn	Phe	Lys	Ala	Gln	Val	Asn	Ser	Ala	Pro
	4535					4540					4545			
Asn	His	Asn	Thr	Leu	Glu	Thr	Ile	Lys	Asn	Lys	Ala	Asp	Thr	Leu
	4550					4555					4560			
Asn	Gln	Ser	Met	Thr	Ala	Leu	Ser	Glu	Ser	Ile	Ala	Asp	Tyr	Glu
	4565					4570					4575			
Asn	Gln	Lys	Gln	Gln	Glu	Asn	Tyr	Leu	Asp	Ala	Ser	Asn	Asn	Lys
	4580					4585					4590			

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Arg	Gln	Asp	Tyr	Asp	Asn	Ala	Val	Asn	Ala	Ala	Lys	Gly	Ile	Leu
4595						4600					4605			
Asn	Gln	Thr	Gln	Ser	Pro	Thr	Met	Ser	Ala	Asp	Val	Ile	Asp	Gln
4610						4615					4620			
Lys	Ala	Glu	Asp	Val	Lys	Arg	Thr	Lys	Thr	Ala	Leu	Asp	Gly	Asn
4625						4630					4635			
Gln	Arg	Leu	Glu	Val	Ala	Lys	Gln	Gln	Ala	Leu	Asn	His	Leu	Asn
4640						4645					4650			
Thr	Leu	Asn	Asp	Leu	Asn	Asp	Ala	Gln	Arg	Gln	Thr	Leu	Thr	Asp
4655						4660					4665			
Thr	Ile	Asn	His	Ser	Pro	Asn	Ile	Asn	Ser	Val	Asn	Gln	Ala	Lys
4670						4675					4680			
Glu	Lys	Ala	Asn	Thr	Val	Asn	Thr	Ala	Met	Thr	Gln	Leu	Lys	Gln
4685						4690					4695			
Thr	Ile	Ala	Asn	Tyr	Asp	Asp	Glu	Leu	His	Asp	Gly	Asn	Tyr	Ile
4700						4705					4710			
Asn	Ala	Asp	Lys	Asp	Lys	Lys	Asp	Ala	Tyr	Asn	Asn	Ala	Val	Asn
4715						4720					4725			
Asn	Ala	Lys	Gln	Leu	Ile	Asn	Gln	Ser	Asp	Ala	Asn	Gln	Ala	Gln
4730						4735					4740			
Leu	Asp	Pro	Ala	Glu	Ile	Asn	Lys	Val	Thr	Gln	Arg	Val	Asn	Thr
4745						4750					4755			
Thr	Lys	Asn	Asp	Leu	Asn	Gly	Asn	Asp	Lys	Leu	Ala	Glu	Ala	Lys
4760						4765					4770			
Arg	Asp	Ala	Asn	Thr	Thr	Ile	Asp	Gly	Leu	Thr	Tyr	Leu	Asn	Glu
4775						4780					4785			

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Ala	Gln	Arg	Asn	Lys	Ala	Lys	Glu	Asn	Val	Gly	Lys	Ala	Ser	Thr
4790						4795					4800			
Lys	Thr	Asn	Ile	Thr	Ser	Gln	Leu	Gln	Asp	Tyr	Asn	Gln	Leu	Asn
4805						4810					4815			
Ile	Ala	Met	Gln	Ala	Leu	Arg	Asn	Ser	Val	Asn	Asp	Val	Asn	Asn
4820						4825					4830			
Val	Lys	Ala	Asn	Ser	Asn	Tyr	Ile	Asn	Glu	Asp	Asn	Gly	Pro	Lys
4835						4840					4845			
Glu	Ala	Tyr	Asn	Gln	Ala	Val	Thr	His	Ala	Gln	Thr	Leu	Ile	Asn
4850						4855					4860			
Ala	Gln	Ser	Asn	Pro	Glu	Met	Ser	Arg	Asp	Val	Val	Asn	Gln	Lys
4865						4870					4875			
Thr	Gln	Ala	Val	Asn	Thr	Ala	His	Gln	Asn	Leu	His	Gly	Gln	Gln
4880						4885					4890			
Lys	Leu	Glu	Gln	Ala	Gln	Ser	Ser	Ala	Asn	Thr	Glu	Ile	Gly	Asn
4895						4900					4905			
Leu	Pro	Asn	Leu	Thr	Asn	Thr	Gln	Lys	Ala	Lys	Glu	Lys	Glu	Leu
4910						4915					4920			
Val	Asn	Ser	Lys	Gln	Thr	Arg	Thr	Glu	Val	Gln	Glu	Gln	Leu	Asn
4925						4930					4935			
Gln	Ala	Lys	Ser	Leu	Asp	Ser	Ser	Met	Gly	Thr	Leu	Lys	Ser	Leu
4940						4945					4950			
Val	Ala	Lys	Gln	Pro	Thr	Val	Gln	Lys	Thr	Ser	Val	Tyr	Ile	Asn
4955						4960					4965			
Glu	Asp	Gln	Pro	Glu	Gln	Ser	Ala	Tyr	Asn	Asp	Ser	Ile	Thr	Met
4970						4975					4980			

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Gly	Gln	Thr	Ile	Ile	Asn	Lys	Thr	Ala	Asp	Pro	Val	Leu	Asp	Lys
4985						4990					4995			
Thr	Leu	Val	Asp	Asn	Ala	Ile	Ser	Asn	Ile	Ser	Thr	Lys	Glu	Asn
5000						5005					5010			
Ala	Leu	His	Gly	Glu	Gln	Lys	Leu	Thr	Thr	Ala	Lys	Thr	Glu	Ala
5015						5020					5025			
Ile	Asn	Ala	Leu	Asn	Thr	Leu	Ala	Asp	Leu	Asn	Thr	Pro	Gln	Lys
5030						5035					5040			
Glu	Ala	Ile	Lys	Thr	Ala	Ile	Asn	Thr	Ala	His	Thr	Arg	Thr	Asp
5045						5050					5055			
Val	Thr	Ala	Glu	Gln	Ser	Lys	Ala	Asn	Gln	Ile	Asn	Ser	Ala	Met
5060						5065					5070			
His	Thr	Leu	Arg	Gln	Asn	Ile	Ser	Asp	Asn	Glu	Ser	Val	Thr	Asn
5075						5080					5085			
Glu	Ser	Asn	Tyr	Ile	Asn	Ala	Glu	Pro	Glu	Lys	Gln	His	Ala	Phe
5090						5095					5100			
Thr	Glu	Ala	Leu	Asn	Asn	Ala	Lys	Glu	Ile	Val	Asn	Glu	Gln	Gln
5105						5110					5115			
Ala	Thr	Leu	Asp	Ala	Asn	Ser	Ile	Asn	Gln	Lys	Ala	Gln	Ala	Ile
5120						5125					5130			
Leu	Thr	Thr	Lys	Asn	Ala	Leu	Asp	Gly	Glu	Glu	Gln	Leu	Arg	Arg
5135						5140					5145			
Ala	Lys	Glu	Asn	Ala	Asp	Gln	Glu	Ile	Asn	Thr	Leu	Asn	Gln	Leu
5150						5155					5160			
Thr	Asp	Ala	Gln	Arg	Asn	Ser	Glu	Lys	Gly	Leu	Val	Asn	Ser	Ser
5165						5170					5175			

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Gln	Thr	Arg	Thr	Glu	Val	Ala	Ser	Gln	Leu	Ala	Lys	Ala	Lys	Glu
5180						5185					5190			
Leu	Asn	Lys	Val	Met	Glu	Gln	Leu	Asn	His	Leu	Ile	Asn	Gly	Lys
5195						5200					5205			
Asn	Gln	Met	Ile	Asn	Ser	Ser	Lys	Phe	Ile	Asn	Glu	Asp	Ala	Asn
5210						5215					5220			
Gln	Gln	Gln	Ala	Tyr	Ser	Asn	Ala	Ile	Ala	Ser	Ala	Glu	Ala	Leu
5225						5230					5235			
Lys	Asn	Lys	Ser	Gln	Asn	Pro	Glu	Leu	Asp	Lys	Val	Thr	Ile	Glu
5240						5245					5250			
Gln	Ala	Ile	Asn	Asn	Ile	Asn	Ser	Ala	Ile	Asn	Asn	Leu	Asn	Gly
5255						5260					5265			
Glu	Ala	Lys	Leu	Thr	Lys	Ala	Lys	Glu	Asp	Ala	Val	Ala	Ser	Ile
5270						5275					5280			
Asn	Asn	Leu	Ser	Gly	Leu	Thr	Asn	Glu	Gln	Lys	Pro	Lys	Glu	Asn
5285						5290					5295			
Gln	Ala	Val	Asn	Gly	Ala	Gln	Thr	Arg	Asp	Gln	Val	Ala	Asn	Lys
5300						5305					5310			
Leu	Arg	Asp	Ala	Glu	Ala	Leu	Asp	Gln	Ser	Met	Gln	Thr	Leu	Arg
5315						5320					5325			
Asp	Leu	Val	Asn	Asn	Gln	Asn	Ala	Ile	His	Ser	Thr	Ser	Asn	Tyr
5330						5335					5340			
Phe	Asn	Glu	Asp	Ser	Thr	Gln	Lys	Asn	Thr	Tyr	Asp	Asn	Ala	Ile
5345						5350					5355			
Asp	Asn	Gly	Ser	Thr	Tyr	Ile	Thr	Gly	Gln	His	Asn	Pro	Glu	Leu
5360						5365					5370			

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Asn	Lys	Ser	Thr	Ile	Asp	Gln	Thr	Ile	Ser	Arg	Ile	Asn	Thr	Ala
	5375					5380					5385			
Lys	Asn	Asp	Leu	His	Gly	Val	Glu	Lys	Leu	Gln	Arg	Asp	Lys	Gly
	5390					5395					5400			
Thr	Ala	Asn	Gln	Glu	Ile	Gly	Gln	Leu	Gly	Tyr	Leu	Asn	Asp	Pro .
	5405					5410					5415			
Gln	Lys	Ser	Gly	Glu	Glu	Ser	Leu	Val	Asn	Gly	Ser	Asn	Thr	Arg
	5420					5425					5430			
Ser	Glu	Val	Glu	Glu	His	Leu	Asn	Glu	Ala	Lys	Ser	Leu	Asn	Asn
	5435					5440					5445			
Ala	Met	Lys	Gln	Leu	Arg	Asp	Lys	Val	Ala	Glu	Lys	Thr	Asn	Val
	5450					5455					5460			
Lys	Gln	Ser	Ser	Asp	Tyr	Ile	Asn	Asp	Ser	Thr	Glu	His	Gln	Arg
	5465					5470					5475			
Gly	Tyr	Asp	Gln	Ala	Leu	Gln	Glu	Ala	Glu	Asn	Ile	Ile	Asn	Glu
	5480					5485					5490			
Ile	Gly	Asn	Pro	Thr	Leu	Asn	Lys	Ser	Glu	Ile	Glu	Gln	Lys	Leu
	5495					5500					5505			
Gln	Gln	Leu	Thr	Asp	Ala	Gln	Asn	Ala	Leu	Gln	Gly	Ser	His	Leu
	5510					5515					5520			
Leu	Glu	Glu	Ala	Lys	Asn	Asn	Ala	Ile	Thr	Gly	Ile	Asn	Lys	Leu
	5525					5530					5535			
Thr	Ala	Leu	Asn	Asp	Ala	Gln	Arg	Gln	Lys	Ala	Ile	Glu	Asn	Val
	5540					5545					5550			
Gln	Ala	Gln	Gln	Thr	Ile	Pro	Ala	Val	Asn	Gln	Gln	Leu	Thr	Leu
	5555					5560					5565			

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Asp	Arg	Glu	Ile	Asn	Thr	Ala	Met	Gln	Ala	Leu	Arg	Asp	Lys	Val
5570						5575					5580			
Gly	Gln	Gln	Asn	Asn	Val	His	Gln	Gln	Ser	Asn	Tyr	Phe	Asn	Glu
5585						5590					5595			
Asp	Glu	Gln	Pro	Lys	His	Asn	Tyr	Asp	Asn	Ser	Val	Gln	Ala	Gly
5600						5605					5610			
Gln	Thr	Ile	Ile	Asp	Lys	Leu	Gln	Asp	Pro	Ile	Met	Asn	Lys	Asn
5615						5620					5625			
Glu	Ile	Glu	Gln	Ala	Ile	Asn	Gln	Ile	Asn	Thr	Thr	Gln	Thr	Ala
5630						5635					5640			
Leu	Ser	Gly	Glu	Asn	Lys	Leu	His	Thr	Asp	Gln	Glu	Ser	Thr	Asn
5645						5650					5655			
Arg	Gln	Ile	Glu	Gly	Leu	Ser	Ser	Leu	Asn	Thr	Ala	Gln	Ile	Asn
5660						5665					5670			
Ala	Glu	Lys	Asp	Leu	Val	Asn	Gln	Ala	Lys	Thr	Arg	Thr	Asp	Val
5675						5680					5685			
Ala	Gln	Lys	Leu	Ala	Ala	Ala	Lys	Glu	Ile	Asn	Ser	Ala	Met	Ser
5690						5695					5700			
Asn	Leu	Arg	Asp	Gly	Ile	Gln	Asn	Lys	Glu	Asp	Ile	Lys	Arg	Ser
5705						5710					5715			
Ser	Ala	Tyr	Ile	Asn	Ala	Asp	Pro	Thr	Lys	Val	Thr	Ala	Tyr	Asp
5720						5725					5730			
Gln	Ala	Leu	Gln	Asn	Ala	Glu	Asn	Ile	Ile	Asn	Ala	Thr	Pro	Asn
5735						5740					5745			
Val	Glu	Leu	Asn	Lys	Ala	Thr	Ile	Glu	Gln	Ala	Leu	Ser	Arg	Val
5750						5755					5760			

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Gln	Gln	Ala	Gln	Gln	Asp	Leu	Asp	Gly	Val	Gln	Gln	Leu	Ala	Asn
5765						5770					5775			
Ala	Lys	Gln	Gln	Ala	Thr	Gln	Thr	Val	Asn	Gly	Leu	Asn	Ser	Leu
5780						5785					5790			
Asn	Asp	Gly	Gln	Lys	Arg	Glu	Leu	Asn	Leu	Leu	Ile	Asn	Ser	Ala
5795						5800					5805			
Asn	Thr	Arg	Thr	Lys	Val	Gln	Glu	Glu	Leu	Asn	Lys	Ala	Thr	Glu
5810						5815					5820			
Leu	Asn	His	Ala	Met	Glu	Ala	Leu	Arg	Asn	Ser	Val	Gln	Asn	Val
5825						5830					5835			
Asp	Gln	Val	Lys	Gln	Ser	Ser	Asn	Tyr	Val	Asn	Glu	Asp	Gln	Pro
5840						5845					5850			
Glu	Gln	His	Asn	Tyr	Asp	Asn	Ala	Val	Asn	Glu	Ala	Gln	Ala	Thr
5855						5860					5865			
Ile	Asn	Asn	Asn	Ala	Gln	Pro	Val	Leu	Asp	Lys	Leu	Ala	Ile	Glu
5870						5875					5880			
Arg	Leu	Thr	Gln	Thr	Val	Asn	Thr	Thr	Lys	Asp	Ala	Leu	His	Gly
5885						5890					5895			
Ala	Gln	Lys	Leu	Thr	Gln	Asp	Gln	Gln	Ala	Ala	Glu	Thr	Gly	Ile
5900						5905					5910			
Arg	Gly	Leu	Thr	Ser	Leu	Asn	Glu	Pro	Gln	Lys	Asn	Ala	Glu	Val
5915						5920					5925			
Ala	Lys	Val	Thr	Ala	Ala	Thr	Thr	Arg	Asp	Glu	Val	Arg	Asn	Ile
5930						5935					5940			
Arg	Gln	Glu	Ala	Thr	Thr	Leu	Asp	Thr	Ala	Met	Leu	Gly	Leu	Arg
5945						5950					5955			

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Lys	Ser	Ile	Lys	Asp	Lys	Asn	Asp	Thr	Lys	Asn	Ser	Ser	Lys	Tyr
	5960					5965					5970			
Ile	Asn	Glu	Asp	His	Asp	Gln	Gln	Gln	Ala	Tyr	Asp	Asn	Ala	Val
	5975					5980					5985			
Asn	Asn	Ala	Gln	Gln	Val	Ile	Asp	Glu	Thr	Gln	Ala	Thr	Leu	Ser
	5990					5995					6000			
Ser	Asp	Thr	Ile	Asn	Gln	Leu	Ala	Asn	Ala	Val	Thr	Gln	Ala	Lys
	6005					6010					6015			
Ser	Asn	Leu	His	Gly	Asp	Thr	Lys	Leu	Gln	His	Asp	Lys	Asp	Ser
	6020					6025					6030			
Ala	Lys	Gln	Thr	Ile	Ala	Gln	Leu	Gln	Asn	Leu	Asn	Ser	Ala	Gln
	6035					6040					6045			
Lys	His	Met	Glu	Asp	Ser	Leu	Ile	Asp	Asn	Glu	Ser	Thr	Arg	Thr
	6050					6055					6060			
Gln	Val	Gln	His	Asp	Leu	Thr	Glu	Ala	Gln	Ala	Leu	Asp	Gly	Leu
	6065					6070					6075			
Met	Gly	Ala	Leu	Lys	Glu	Ser	Ile	Lys	Asp	Tyr	Thr	Asn	Ile	Val
	6080					6085					6090			
Ser	Asn	Gly	Asn	Tyr	Ile	Asn	Ala	Glu	Pro	Ser	Lys	Lys	Gln	Ala
	6095					6100					6105			
Tyr	Asp	Ala	Ala	Val	Gln	Asn	Ala	Gln	Asn	Ile	Ile	Asn	Gly	Thr
	6110					6115					6120			
Asn	Gln	Pro	Thr	Ile	Asn	Lys	Gly	Asn	Val	Thr	Thr	Ala	Thr	Gln
	6125					6130					6135			
Thr	Val	Lys	Asn	Thr	Lys	Asp	Ala	Leu	Asp	Gly	Asp	His	Arg	Leu
	6140					6145					6150			

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Glu	Glu	Ala	Lys	Asn	Asn	Ala	Asn	Gln	Thr	Ile	Arg	Asn	Leu	Ser
6155						6160					6165			
Asn	Leu	Asn	Asn	Ala	Gln	Lys	Asp	Ala	Glu	Lys	Asn	Leu	Val	Asn
6170						6175					6180			
Ser	Ala	Ser	Thr	Leu	Glu	Gln	Val	Gln	Gln	Asn	Leu	Gln	Thr	Ala
6185						6190					6195			
Gln	Gln	Leu	Asp	Asn	Ala	Met	Gly	Glu	Leu	Arg	Gln	Ser	Ile	Ala
6200						6205					6210			
Lys	Lys	Asp	Gln	Val	Lys	Ala	Asp	Ser	Lys	Tyr	Leu	Asn	Glu	Asp
6215						6220					6225			
Pro	Gln	Ile	Lys	Gln	Asn	Tyr	Asp	Asp	Ala	Val	Gln	Arg	Val	Glu
6230						6235					6240			
Thr	Ile	Ile	Asn	Glu	Thr	Gln	Asn	Pro	Glu	Leu	Leu	Lys	Ala	Asn
6245						6250					6255			
Ile	Asp	Gln	Ala	Thr	Gln	Ser	Val	Gln	Asn	Ala	Glu	Gln	Ala	Leu
6260						6265					6270			
His	Gly	Ala	Glu	Lys	Leu	Asn	Gln	Asp	Lys	Gln	Thr	Ser	Ser	Thr
6275						6280					6285			
Glu	Leu	Asp	Gly	Leu	Thr	Asp	Leu	Thr	Asp	Ala	Gln	Arg	Glu	Lys
6290						6295					6300			
Leu	Arg	Glu	Gln	Ile	Asn	Thr	Ser	Asn	Ser	Arg	Asp	Asp	Ile	Lys
6305						6310					6315			
Gln	Lys	Ile	Glu	Gln	Ala	Lys	Ala	Leu	Asn	Asp	Ala	Met	Lys	Lys
6320						6325					6330			
Leu	Lys	Glu	Gln	Val	Ala	Gln	Lys	Asp	Gly	Val	His	Ala	Asn	Ser
6335						6340					6345			

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Asp	Tyr	Thr	Asn	Glu	Asp	Ser	Ala	Gln	Lys	Asp	Ala	Tyr	Asn	Asn
6350						6355					6360			
Ala	Leu	Lys	Gln	Ala	Glu	Asp	Ile	Ile	Asn	Asn	Ser	Ser	Asn	Pro
6365						6370					6375			
Asn	Leu	Asn	Ala	Gln	Asp	Ile	Thr	Asn	Ala	Leu	Asn	Asn	Ile	Lys
6380						6385					6390			
Gln	Ala	Gln	Asp	Asn	Leu	His	Gly	Ala	Gln	Lys	Leu	Gln	Gln	Asp
6395						6400					6405			
Lys	Asn	Thr	Thr	Asn	Gln	Ala	Ile	Gly	Asn	Leu	Asn	His	Leu	Asn
6410						6415					6420			
Gln	Pro	Gln	Lys	Asp	Ala	Leu	Ile	Gln	Ala	Ile	Asn	Gly	Ala	Thr
6425						6430					6435			
Ser	Arg	Asp	Gln	Val	Ala	Glu	Lys	Leu	Lys	Glu	Ala	Glu	Ala	Leu
6440						6445					6450			
Asp	Glu	Ala	Met	Lys	Gln	Leu	Glu	Asp	Gln	Val	Asn	Gln	Asp	Asp
6455						6460					6465			
Gln	Ile	Ser	Asn	Ser	Ser	Pro	Phe	Ile	Asn	Glu	Asp	Ser	Asp	Lys
6470						6475					6480			
Gln	Lys	Thr	Tyr	Asn	Asp	Lys	Ile	Gln	Ala	Ala	Lys	Glu	Ile	Ile
6485						6490					6495			
Asn	Gln	Thr	Ser	Asn	Pro	Thr	Leu	Asp	Lys	Gln	Lys	Ile	Ala	Asp
6500						6505					6510			
Thr	Leu	Gln	Asn	Ile	Lys	Asp	Ala	Val	Asn	Asn	Leu	His	Gly	Asp
6515						6520					6525			
Gln	Lys	Leu	Ala	Gln	Ser	Lys	Gln	Asp	Ala	Asn	Asn	Gln	Leu	Asn
6530						6535					6540			

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His	Leu	Asp	Asp	Leu	Thr	Glu	Glu	Gln	Lys	Asn	His	Phe	Lys	Pro
	6545					6550					6555			
Leu	Ile	Asn	Asn	Ala	Asp	Thr	Arg	Asp	Glu	Val	Asn	Lys	Gln	Leu
	6560					6565					6570			
Glu	Ile	Ala	Lys	Gln	Leu	Asn	Gly	Asp	Met	Ser	Thr	Leu	His	Lys
	6575					6580					6585			
Val	Ile	Asn	Asp	Lys	Asp	Gln	Ile	Gln	His	Leu	Ser	Asn	Tyr	Ile
	6590					6595					6600			
Asn	Ala	Asp	Asn	Asp	Lys	Lys	Gln	Asn	Tyr	Asp	Asn	Ala	Ile	Lys
	6605					6610					6615			
Glu	Ala	Glu	Asp	Leu	Ile	His	Asn	His	Pro	Asp	Thr	Leu	Asp	His
	6620					6625					6630			
Lys	Ala	Leu	Gln	Asp	Leu	Leu	Asn	Lys	Ile	Asp	Gln	Ala	His	Asn
	6635					6640					6645			
Glu	Leu	Asn	Gly	Glu	Ser	Arg	Phe	Lys	Gln	Ala	Leu	Asp	Asn	Ala
	6650					6655					6660			
Leu	Asn	Asp	Ile	Asp	Ser	Leu	Asn	Ser	Leu	Asn	Val	Pro	Gln	Arg
	6665					6670					6675			
Gln	Thr	Val	Lys	Asp	Asn	Ile	Asn	His	Val	Thr	Thr	Leu	Glu	Ser
	6680					6685					6690			
Leu	Ala	Gln	Glu	Leu	Gln	Lys	Ala	Lys	Glu	Leu	Asn	Asp	Ala	Met
	6695					6700					6705			
Lys	Ala	Met	Arg	Asp	Ser	Ile	Met	Asn	Gln	Glu	Gln	Ile	Arg	Lys
	6710					6715					6720			
Asn	Ser	Asn	Tyr	Thr	Asn	Glu	Asp	Leu	Ala	Gln	Gln	Asn	Ala	Tyr
	6725					6730					6735			

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Asn	His	Ala	Val	Asp	Lys	Ile	Asn	Asn	Ile	Ile	Gly	Glu	Asp	Asn
	6740					6745					6750			
Ala	Thr	Met	Asp	Pro	Gln	Ile	Ile	Lys	Gln	Ala	Thr	Gln	Asp	Ile
	6755					6760					6765			
Asn	Thr	Ala	Ile	Asn	Gly	Leu	Asn	Gly	Asp	Gln	Lys	Leu	Gln	Asp
	6770					6775					6780			
Ala	Lys	Thr	Asp	Ala	Lys	Gln	Gln	Ile	Thr	Asn	Phe	Thr	Gly	Leu
	6785					6790					6795			
Thr	Glu	Pro	Gln	Lys	Gln	Ala	Leu	Glu	Asn	Ile	Ile	Asn	Gln	Gln
	6800					6805					6810			
Thr	Ser	Arg	Ala	Asn	Val	Ala	Lys	Gln	Leu	Ser	His	Ala	Lys	Phe
	6815					6820					6825			
Leu	Asn	Gly	Lys	Met	Glu	Glu	Leu	Lys	Val	Ala	Val	Ala	Lys	Ala
	6830					6835					6840			
Ser	Leu	Val	Arg	Gln	Asn	Ser	Asn	Tyr	Ile	Asn	Glu	Asp	Val	Ser
	6845					6850					6855			
Glu	Lys	Glu	Ala	Tyr	Glu	Gln	Ala	Ile	Ala	Lys	Gly	Gln	Glu	Ile
	6860					6865					6870			
Ile	Asn	Ser	Glu	Asn	Asn	Pro	Thr	Ile	Ser	Ser	Thr	Asp	Ile	Asn
	6875					6880					6885			
Arg	Thr	Ile	Gln	Glu	Ile	Asn	Asp	Ala	Glu	Gln	Asn	Leu	His	Gly
	6890					6895					6900			
Asp	Asn	Lys	Leu	Arg	Gln	Ala	Gln	Glu	Ile	Ala	Lys	Asn	Glu	Ile
	6905					6910					6915			
Gln	Asn	Leu	Asp	Gly	Leu	Asn	Ser	Ala	Gln	Ile	Thr	Lys	Leu	Ile
	6920					6925					6930			

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Gln	Asp	Ile	Gly	Arg	Thr	Thr	Thr	Lys	Pro	Ala	Val	Thr	Gln	Lys
	6935					6940					6945			
Leu	Glu	Glu	Ala	Lys	Ala	Ile	Asn	Gln	Ala	Met	Gln	Gln	Leu	Lys
	6950					6955					6960			
Gln	Ser	Ile	Ala	Asp	Lys	Asp	Ala	Thr	Leu	Asn	Ser	Ser	Asn	Tyr
	6965					6970					6975			
Leu	Asn	Glu	Asp	Ser	Glu	Lys	Lys	Leu	Ala	Tyr	Asp	Asn	Ala	Val
	6980					6985					6990			
Ser	Gln	Ala	Glu	Gln	Leu	Ile	Asn	Gln	Leu	Asn	Asp	Pro	Thr	Met
	6995					7000					7005			
Asp	Ile	Ser	Asn	Ile	Gln	Ala	Ile	Thr	Gln	Lys	Val	Ile	Gln	Ala
	7010					7015					7020			
Lys	Asp	Ser	Leu	His	Gly	Ala	Asn	Lys	Leu	Ala	Gln	Asn	Gln	Ala
	7025					7030					7035			
Asp	Ser	Asn	Leu	Ile	Ile	Asn	Gln	Ser	Thr	Asn	Leu	Asn	Asp	Lys
	7040					7045					7050			
Gln	Lys	Gln	Ala	Leu	Asn	Asp	Leu	Ile	Asn	His	Ala	Gln	Thr	Lys
	7055					7060					7065			
Gln	Gln	Val	Ala	Glu	Ile	Ile	Ala	Gln	Ala	Asn	Lys	Leu	Asn	Asn
	7070					7075					7080			
Glu	Met	Gly	Thr	Leu	Lys	Thr	Leu	Val	Glu	Glu	Gln	Ser	Asn	Val
	7085					7090					7095			
His	Gln	Gln	Ser	Lys	Tyr	Ile	Asn	Glu	Asp	Pro	Gln	Val	Gln	Asn
	7100					7105					7110			
Ile	Tyr	Asn	Asp	Ser	Ile	Gln	Lys	Gly	Arg	Glu	Ile	Leu	Asn	Gly
	7115					7120					7125			

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Thr	Thr	Asp	Asp	Val	Leu	Asn	Asn	Asn	Lys	Ile	Ala	Asp	Ala	Ile
	7130					7135					7140			
Gln	Asn	Ile	His	Leu	Thr	Lys	Asn	Asp	Leu	His	Gly	Asp	Gln	Lys
	7145					7150					7155			
Leu	Gln	Lys	Ala	Gln	Gln	Asp	Ala	Thr	Asn	Glu	Leu	Asn	Tyr	Leu
	7160					7165					7170			
Thr	Asn	Leu	Asn	Asn	Ser	Gln	Arg	Gln	Ser	Glu	His	Asp	Glu	Ile
	7175					7180					7185			
Asn	Ser	Ala	Pro	Ser	Arg	Thr	Glu	Val	Ser	Asn	Asp	Leu	Asn	His
	7190					7195					7200			
Ala	Lys	Ala	Leu	Asn	Glu	Ala	Met	Arg	Gln	Leu	Glu	Asn	Glu	Val
	7205					7210					7215			
Ala	Leu	Glu	Asn	Ser	Val	Lys	Lys	Leu	Ser	Asp	Phe	Ile	Asn	Glu
	7220					7225					7230			
Asp	Glu	Ala	Ala	Gln	Asn	Glu	Tyr	Ser	Asn	Ala	Leu	Gln	Lys	Ala
	7235					7240					7245			
Lys	Asp	Ile	Ile	Asn	Gly	Val	Pro	Ser	Ser	Thr	Leu	Asp	Lys	Ala
	7250					7255					7260			
Thr	Ile	Glu	Asp	Ala	Leu	Leu	Glu	Leu	Gln	Asn	Ala	Arg	Glu	Ser
	7265					7270					7275			
Leu	His	Gly	Glu	Gln	Lys	Leu	Gln	Glu	Ala	Lys	Asn	Gln	Ala	Val
	7280					7285					7290			
Ala	Glu	Ile	Asp	Asn	Leu	Gln	Ala	Leu	Asn	Pro	Gly	Gln	Val	Leu
	7295					7300					7305			
Ala	Glu	Lys	Thr	Leu	Val	Asn	Gln	Ala	Ser	Thr	Lys	Pro	Glu	Val
	7310					7315					7320			

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Gln	Glu	Ala	Leu	Gln	Lys	Ala	Lys	Glu	Leu	Asn	Glu	Ala	Met	Lys
	7325					7330					7335			
Ala	Leu	Lys	Thr	Glu	Ile	Asn	Lys	Lys	Glu	Gln	Ile	Lys	Ala	Asp
	7340					7345					7350			
Ser	Arg	Tyr	Val	Asn	Ala	Asp	Ser	Gly	Leu	Gln	Ala	Asn	Tyr	Asn
	7355					7360					7365			
Ser	Ala	Leu	Asn	Tyr	Gly	Ser	Gln	Ile	Ile	Ala	Thr	Thr	Gln	Pro
	7370					7375					7380			
Pro	Glu	Leu	Asn	Lys	Asp	Val	Ile	Asn	Arg	Ala	Thr	Gln	Thr	Ile
	7385					7390					7395			
Lys	Thr	Ala	Glu	Asn	Asn	Leu	Asn	Gly	Gln	Ser	Lys	Leu	Ala	Glu
	7400					7405					7410			
Ala	Lys	Ser	Asp	Gly	Asn	Gln	Ser	Ile	Glu	His	Leu	Gln	Gly	Leu
	7415					7420					7425			
Thr	Gln	Ser	Gln	Lys	Asp	Lys	Gln	His	Asp	Leu	Ile	Asn	Gln	Ala
	7430					7435					7440			
Gln	Thr	Lys	Gln	Gln	Val	Asp	Asp	Ile	Val	Asn	Asn	Ser	Lys	Gln
	7445					7450					7455			
Leu	Asp	Asn	Ser	Met	Asn	Gln	Leu	Gln	Gln	Ile	Val	Asn	Asn	Asp
	7460					7465					7470			
Asn	Thr	Val	Lys	Gln	Asn	Ser	Asp	Phe	Ile	Asn	Glu	Asp	Ser	Ser
	7475					7480					7485			
Gln	Gln	Asp	Ala	Tyr	Asn	His	Ala	Ile	Gln	Ala	Ala	Lys	Asp	Leu
	7490					7495					7500			
Ile	Thr	Ala	His	Pro	Thr	Ile	Met	Asp	Lys	Asn	Gln	Ile	Asp	Gln
	7505					7510					7515			

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Ala	Ile	Glu	Asn	Ile	Lys	Gln	Ala	Leu	Asn	Asp	Leu	His	Gly	Ser
7520						7525					7530			
Asn	Lys	Leu	Ser	Glu	Asp	Lys	Lys	Glu	Ala	Ser	Glu	Gln	Leu	Gln
7535						7540					7545			
Asn	Leu	Asn	Ser	Leu	Thr	Asn	Gly	Gln	Lys	Asp	Thr	Ile	Leu	Asn
7550						7555					7560			
His	Ile	Phe	Ser	Ala	Pro	Thr	Arg	Ser	Gln	Val	Gly	Glu	Lys	Ile
7565						7570					7575			
Ala	Ser	Ala	Lys	Gln	Leu	Asn	Asn	Thr	Met	Lys	Ala	Leu	Arg	Asp
7580						7585					7590			
Ser	Ile	Ala	Asp	Asn	Asn	Glu	Ile	Leu	Gln	Ser	Ser	Lys	Tyr	Phe
7595						7600					7605			
Asn	Glu	Asp	Ser	Glu	Gln	Gln	Asn	Ala	Tyr	Asn	Gln	Ala	Val	Asn
7610						7615					7620			
Lys	Ala	Lys	Asn	Ile	Ile	Asn	Asp	Gln	Pro	Thr	Pro	Val	Met	Ala
7625						7630					7635			
Asn	Asp	Glu	Ile	Gln	Ser	Val	Leu	Asn	Glu	Val	Lys	Gln	Thr	Lys
7640						7645					7650			
Asp	Asn	Leu	His	Gly	Asp	Gln	Lys	Leu	Ala	Asn	Asp	Lys	Thr	Asp
7655						7660					7665			
Ala	Gln	Ala	Thr	Leu	Asn	Ala	Leu	Asn	Tyr	Leu	Asn	Gln	Ala	Gln
7670						7675					7680			
Arg	Gly	Asn	Leu	Glu	Thr	Lys	Val	Gln	Asn	Ser	Asn	Ser	Arg	Pro
7685						7690					7695			
Glu	Val	Gln	Lys	Val	Val	Gln	Leu	Ala	Asn	Gln	Leu	Asn	Asp	Ala
7700						7705					7710			

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Met	Lys	Lys	Leu	Asp	Asp	Ala	Leu	Thr	Gly	Asn	Asp	Ala	Ile	Lys
	7715					7720					7725			
Gln	Thr	Ser	Asn	Tyr	Ile	Asn	Glu	Asp	Thr	Ser	Gln	Gln	Val	Asn
	7730					7735					7740			
Phe	Asp	Glu	Tyr	Thr	Asp	Arg	Gly	Lys	Asn	Ile	Val	Ala	Glu	Gln
	7745					7750					7755			
Thr	Asn	Pro	Asn	Met	Ser	Pro	Thr	Asn	Ile	Asn	Thr	Ile	Ala	Asp
	7760					7765					7770			
Lys	Ile	Thr	Glu	Ala	Lys	Asn	Asp	Leu	His	Gly	Val	Gln	Lys	Leu
	7775					7780					7785			
Lys	Gln	Ala	Gln	Gln	Gln	Ser	Ile	Asn	Thr	Ile	Asn	Gln	Met	Thr
	7790					7795					7800			
Gly	Leu	Asn	Gln	Ala	Gln	Lys	Glu	Gln	Leu	Asn	Gln	Glu	Ile	Gln
	7805					7810					7815			
Gln	Thr	Gln	Thr	Arg	Ser	Glu	Val	His	Gln	Val	Ile	Asn	Lys	Ala
	7820					7825					7830			
Gln	Ala	Leu	Asn	Asp	Ser	Met	Asn	Thr	Leu	Arg	Gln	Ser	Ile	Thr
	7835					7840					7845			
Asp	Glu	His	Glu	Val	Lys	Gln	Thr	Ser	Asn	Tyr	Ile	Asn	Glu	Thr
	7850					7855					7860			
Val	Gly	Asn	Gln	Thr	Ala	Tyr	Asn	Asn	Ala	Val	Asp	Arg	Val	Lys
	7865					7870					7875			
Gln	Ile	Ile	Asn	Gln	Thr	Ser	Asn	Pro	Thr	Met	Asn	Pro	Leu	Glu
	7880					7885					7890			
Val	Glu	Arg	Ala	Thr	Ser	Asn	Val	Lys	Ile	Ser	Lys	Asp	Ala	Leu
	7895					7900					7905			

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His	Gly 7910	Glu	Arg	Glu	Leu	Asn 7915	Asp	Asn	Lys	Asn	Ser 7920	Lys	Thr	Phe
Ala	Val 7925	Asn	His	Leu	Asp	Asn 7930	Leu	Asn	Gln	Ala	Gln 7935	Lys	Glu	Ala
Leu	Thr 7940	His	Glu	Ile	Glu	Gln 7945	Ala	Thr	Ile	Val	Ser 7950	Gln	Val	Asn
Asn	Ile 7955	Tyr	Asn	Lys	Ala	Lys 7960	Ala	Leu	Asn	Asn	Asp 7965	Met	Lys	Lys
Leu	Lys 7970	Asp	Ile	Val	Ala	Gln 7975	Gln	Asp	Asn	Val	Arg 7980	Gln	Ser	Asn
Asn	Tyr 7985	Ile	Asn	Glu	Asp	Ser 7990	Thr	Pro	Gln	Asn	Met 7995	Tyr	Asn	Asp
Thr	Ile 8000	Asn	His	Ala	Gln	Ser 8005	Ile	Ile	Asp	Gln	Val 8010	Ala	Asn	Pro
Thr	Met 8015	Ser	His	Asp	Glu	Ile 8020	Glu	Asn	Ala	Ile	Asn 8025	Asn	Ile	Lys
His	Ala 8030	Ile	Asn	Ala	Leu	Asp 8035	Gly	Glu	His	Lys	Leu 8040	Gln	Gln	Ala
Lys	Glu 8045	Asn	Ala	Asn	Leu	Leu 8050	Ile	Asn	Ser	Leu	Asn 8055	Asp	Leu	Asn
Ala	Pro 8060	Gln	Arg	Asp	Ala	Ile 8065	Asn	Arg	Leu	Val	Asn 8070	Glu	Ala	Gln
Thr	Arg 8075	Glu	Lys	Val	Ala	Glu 8080	Gln	Leu	Gln	Ser	Ala 8085	Gln	Ala	Leu
Asn	Asp 8090	Ala	Met	Lys	His	Leu 8095	Arg	Asn	Ser	Ile	Gln 8100	Asn	Gln	Ser

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Ser	Val	Arg	Gln	Glu	Ser	Lys	Tyr	Ile	Asn	Ala	Ser	Asp	Ala	Lys
8105						8110					8115			
Lys	Glu	Gln	Tyr	Asn	His	Ala	Val	Arg	Glu	Val	Glu	Asn	Ile	Ile
8120						8125					8130			
Asn	Glu	Gln	His	Pro	Thr	Leu	Asp	Lys	Glu	Ile	Ile	Lys	Gln	Leu
8135						8140					8145			
Thr	Asp	Gly	Val	Asn	Gln	Ala	Asn	Asn	Asp	Leu	Asn	Gly	Val	Glu
8150						8155					8160			
Leu	Leu	Asp	Ala	Asp	Lys	Gln	Asn	Ala	His	Gln	Ser	Ile	Pro	Thr
8165						8170					8175			
Leu	Met	His	Leu	Asn	Gln	Ala	Gln	Gln	Asn	Ala	Leu	Asn	Glu	Lys
8180						8185					8190			
Ile	Asn	Asn	Ala	Val	Thr	Arg	Thr	Glu	Val	Ala	Ala	Ile	Ile	Gly
8195						8200					8205			
Gln	Ala	Lys	Leu	Leu	Asp	His	Ala	Met	Glu	Asn	Leu	Glu	Glu	Ser
8210						8215					8220			
Ile	Lys	Asp	Lys	Glu	Gln	Val	Lys	Gln	Ser	Ser	Asn	Tyr	Ile	Asn
8225						8230					8235			
Glu	Asp	Ser	Asp	Val	Gln	Glu	Thr	Tyr	Asp	Asn	Ala	Val	Asp	His
8240						8245					8250			
Val	Thr	Glu	Ile	Leu	Asn	Gln	Thr	Val	Asn	Pro	Thr	Leu	Ser	Ile
8255						8260					8265			
Glu	Asp	Ile	Glu	His	Ala	Ile	Asn	Glu	Val	Asn	Gln	Ala	Lys	Lys
8270						8275					8280			
Gln	Leu	Arg	Gly	Lys	Gln	Lys	Leu	Tyr	Gln	Thr	Ile	Asp	Leu	Ala
8285						8290					8295			

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Asp	Lys	Glu	Leu	Ser	Lys	Leu	Asp	Asp	Leu	Thr	Ser	Gln	Gln	Ser
	8300					8305					8310			
Ser	Ser	Ile	Ser	Asn	Gln	Ile	Tyr	Thr	Ala	Lys	Thr	Arg	Thr	Glu
	8315					8320					8325			
Val	Ala	Gln	Ala	Ile	Glu	Lys	Ala	Lys	Ser	Leu	Asn	His	Ala	Met
	8330					8335					8340			
Lys	Ala	Leu	Asn	Lys	Val	Tyr	Lys	Asn	Ala	Asp	Lys	Val	Leu	Asp
	8345					8350					8355			
Ser	Ser	Arg	Phe	Ile	Asn	Glu	Asp	Gln	Pro	Glu	Lys	Lys	Ala	Tyr
	8360					8365					8370			
Gln	Gln	Ala	Ile	Asn	His	Val	Asp	Ser	Ile	Ile	His	Arg	Gln	Thr
	8375					8380					8385			
Asn	Pro	Glu	Met	Asp	Pro	Thr	Val	Ile	Asn	Ser	Ile	Thr	His	Glu
	8390					8395					8400			
Leu	Glu	Thr	Ala	Gln	Asn	Asn	Leu	His	Gly	Asp	Gln	Lys	Leu	Ala
	8405					8410					8415			
His	Ala	Gln	Gln	Asp	Ala	Ala	Asn	Val	Ile	Asn	Gly	Leu	Ile	His
	8420					8425					8430			
Leu	Asn	Val	Ala	Gln	Arg	Glu	Val	Met	Ile	Asn	Thr	Asn	Thr	Asn
	8435					8440					8445			
Ala	Thr	Thr	Arg	Glu	Lys	Val	Ala	Lys	Asn	Leu	Asp	Asn	Ala	Gln
	8450					8455					8460			
Ala	Leu	Asp	Lys	Ala	Met	Glu	Thr	Leu	Gln	Gln	Val	Val	Ala	His
	8465					8470					8475			
Lys	Asn	Asn	Ile	Leu	Asn	Asp	Ser	Lys	Tyr	Leu	Asn	Glu	Asp	Ser
	8480					8485					8490			

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Lys	Tyr	Gln	Gln	Gln	Tyr	Asp	Arg	Val	Ile	Ala	Asp	Ala	Glu	Gln
8495						8500					8505			
Leu	Leu	Asn	Gln	Thr	Thr	Asn	Pro	Thr	Leu	Glu	Pro	Tyr	Lys	Val
8510						8515					8520			
Asp	Ile	Val	Lys	Asp	Asn	Val	Leu	Ala	Asn	Glu	Lys	Ile	Leu	Phe
8525						8530					8535			
Gly	Ala	Glu	Lys	Leu	Ser	Tyr	Asp	Lys	Ser	Asn	Ala	Asn	Asp	Glu
8540						8545					8550			
Ile	Lys	His	Met	Asn	Tyr	Leu	Asn	Asn	Ala	Gln	Lys	Gln	Ser	Ile
8555						8560					8565			
Lys	Asp	Met	Ile	Ser	His	Ala	Ala	Leu	Arg	Thr	Glu	Val	Lys	Gln
8570						8575					8580			
Leu	Leu	Gln	Gln	Ala	Lys	Ile	Leu	Asp	Glu	Ala	Met	Lys	Ser	Leu
8585						8590					8595			
Glu	Asp	Lys	Thr	Gln	Val	Val	Ile	Thr	Asp	Thr	Thr	Leu	Pro	Asn
8600						8605					8610			
Tyr	Thr	Glu	Ala	Ser	Glu	Asp	Lys	Lys	Glu	Lys	Val	Asp	Gln	Thr
8615						8620					8625			
Val	Ser	His	Ala	Gln	Ala	Ile	Ile	Asp	Lys	Ile	Asn	Gly	Ser	Asn
8630						8635					8640			
Val	Ser	Leu	Asp	Gln	Val	Arg	Gln	Ala	Leu	Glu	Gln	Leu	Thr	Gln
8645						8650					8655			
Ala	Ser	Glu	Asn	Leu	Asp	Gly	Asp	Gln	Arg	Val	Glu	Glu	Ala	Lys
8660						8665					8670			
Val	His	Ala	Asn	Gln	Thr	Ile	Asp	Gln	Leu	Thr	His	Leu	Asn	Ser
8675						8680					8685			

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Leu	Gln	Gln	Gln	Thr	Ala	Lys	Glu	Ser	Val	Lys	Asn	Ala	Thr	Lys
	8690					8695					8700			
Leu	Glu	Glu	Ile	Ala	Thr	Val	Ser	Asn	Asn	Ala	Gln	Ala	Leu	Asn
	8705					8710					8715			
Lys	Val	Met	Gly	Lys	Leu	Glu	Gln	Phe	Ile	Asn	His	Ala	Asp	Ser
	8720					8725					8730			
Val	Glu	Asn	Ser	Asp	Asn	Tyr	Arg	Gln	Ala	Asp	Asp	Asp	Lys	Ile
	8735					8740					8745			
Ile	Ala	Tyr	Asp	Glu	Ala	Leu	Glu	His	Gly	Gln	Asp	Ile	Gln	Lys
	8750					8755					8760			
Thr	Asn	Ala	Thr	Gln	Asn	Glu	Thr	Lys	Gln	Ala	Leu	Gln	Gln	Leu
	8765					8770					8775			
Ile	Tyr	Ala	Glu	Thr	Ser	Leu	Asn	Gly	Phe	Glu	Arg	Leu	Asn	His
	8780					8785					8790			
Ala	Arg	Pro	Arg	Ala	Leu	Glu	Tyr	Ile	Lys	Ser	Leu	Glu	Lys	Ile
	8795					8800					8805			
Asn	Asn	Ala	Gln	Lys	Ser	Ala	Leu	Glu	Asp	Lys	Val	Thr	Gln	Ser
	8810					8815					8820			
His	Asp	Leu	Leu	Glu	Leu	Glu	His	Ile	Val	Asn	Glu	Gly	Thr	Asn
	8825					8830					8835			
Leu	Asn	Asp	Ile	Met	Gly	Glu	Leu	Ala	Asn	Ala	Ile	Val	Asn	Asn
	8840					8845					8850			
Tyr	Ala	Pro	Thr	Lys	Ala	Ser	Ile	Asn	Tyr	Ile	Asn	Ala	Asp	Asn
	8855					8860					8865			
Leu	Arg	Lys	Asp	Asn	Phe	Thr	Gln	Ala	Ile	Asn	Asn	Ala	Arg	Asp
	8870					8875					8880			

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Ala	Leu	Asn	Lys	Thr	Gln	Gly	Gln	Asn	Leu	Asp	Phe	Asn	Ala	Ile
	8885					8890					8895			
Asp	Thr	Phe	Lys	Asp	Asp	Ile	Phe	Lys	Thr	Lys	Asp	Ala	Leu	Asn
	8900					8905					8910			
Gly	Ile	Glu	Arg	Leu	Thr	Ala	Ala	Lys	Ser	Lys	Ala	Glu	Lys	Leu
	8915					8920					8925			
Ile	Asp	Ser	Leu	Lys	Phe	Ile	Asn	Lys	Ala	Gln	Phe	Thr	His	Ala
	8930					8935					8940			
Asn	Asp	Glu	Ile	Ile	Asn	Thr	Asn	Ser	Ile	Ala	Gln	Leu	Ser	Arg
	8945					8950					8955			
Ile	Val	Asn	Gln	Ala	Phe	Asp	Leu	Asn	Asp	Ala	Met	Lys	Ser	Leu
	8960					8965					8970			
Arg	Asp	Glu	Leu	Asn	Asn	Gln	Ala	Phe	Pro	Val	Gln	Ala	Ser	Ser
	8975					8980					8985			
Asn	Tyr	Ile	Asn	Ser	Asp	Glu	Asp	Leu	Lys	Gln	Gln	Phe	Asp	His
	8990					8995					9000			
Ala	Leu	Ser	Asn	Ala	Arg	Lys	Val	Leu	Ala	Lys	Glu	Asn	Gly	Lys
	9005					9010					9015			
Asn	Leu	Asp	Glu	Lys	Gln	Ile	Gln	Gly	Leu	Lys	Gln	Val	Ile	Glu
	9020					9025					9030			
Asp	Thr	Lys	Asp	Ala	Leu	Asn	Gly	Ile	Gln	Arg	Leu	Ser	Lys	Ala
	9035					9040					9045			
Lys	Ala	Lys	Ala	Ile	Gln	Tyr	Val	Gln	Ser	Leu	Ser	Tyr	Ile	Asn
	9050					9055					9060			
Asp	Ala	Gln	Arg	His	Ile	Ala	Glu	Asn	Asn	Ile	His	Asn	Ser	Asp
	9065					9070					9075			

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Asp	Leu	Ser	Ser	Leu	Ala	Asn	Thr	Leu	Ser	Lys	Ala	Ser	Asp	Leu
	9080					9085					9090			
Asp	Asn	Ala	Met	Lys	Asp	Leu	Arg	Asp	Thr	Ile	Glu	Ser	Asn	Ser
	9095					9100					9105			
Thr	Ser	Val	Pro	Asn	Ser	Val	Asn	Tyr	Ile	Asn	Ala	Asp	Lys	Asn
	9110					9115					9120			
Leu	Gln	Ile	Glu	Phe	Asp	Glu	Ala	Leu	Gln	Gln	Ala	Ser	Ala	Thr
	9125					9130					9135			
Ser	Ser	Lys	Thr	Ser	Glu	Asn	Pro	Ala	Thr	Ile	Glu	Glu	Val	Leu
	9140					9145					9150			
Gly	Leu	Ser	Gln	Ala	Ile	Tyr	Asp	Thr	Lys	Asn	Ala	Leu	Asn	Gly
	9155					9160					9165			
Glu	Gln	Arg	Leu	Ala	Thr	Glu	Lys	Ser	Lys	Asp	Leu	Lys	Leu	Ile
	9170					9175					9180			
Lys	Gly	Leu	Lys	Asp	Leu	Asn	Lys	Ala	Gln	Leu	Glu	Asp	Val	Thr
	9185					9190					9195			
Asn	Lys	Val	Asn	Ser	Ala	Asn	Thr	Leu	Thr	Glu	Leu	Ser	Gln	Leu
	9200					9205					9210			
Thr	Gln	Ser	Thr	Leu	Glu	Leu	Asn	Asp	Lys	Met	Lys	Leu	Leu	Arg
	9215					9220					9225			
Asp	Lys	Leu	Lys	Thr	Leu	Val	Asn	Pro	Val	Lys	Ala	Ser	Leu	Asn
	9230					9235					9240			
Tyr	Arg	Asn	Ala	Asp	Tyr	Asn	Leu	Lys	Arg	Gln	Phe	Asn	Lys	Ala
	9245					9250					9255			
Leu	Lys	Glu	Ala	Lys	Gly	Val	Leu	Asn	Lys	Asn	Ser	Gly	Thr	Asn
	9260					9265					9270			

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Val	Asn	Ile	Asn	Asp	Ile	Gln	His	Leu	Leu	Thr	Gln	Ile	Asp	Asn
	9275					9280					9285			
Ala	Lys	Asp	Gln	Leu	Asn	Gly	Glu	Arg	Arg	Leu	Lys	Glu	His	Gln
	9290					9295					9300			
Gln	Lys	Ser	Glu	Val	Phe	Ile	Ile	Lys	Glu	Leu	Asp	Ile	Leu	Asn
	9305					9310					9315			
Asn	Ala	Gln	Lys	Ala	Ala	Ile	Ile	Asn	Gln	Ile	Arg	Ala	Ser	Lys
	9320					9325					9330			
Asp	Ile	Lys	Ile	Ile	Asn	Gln	Ile	Val	Asp	Asn	Ala	Ile	Glu	Leu
	9335					9340					9345			
Asn	Asp	Ala	Met	Gln	Gly	Leu	Lys	Glu	His	Val	Ala	Gln	Leu	Thr
	9350					9355					9360			
Ala	Thr	Thr	Lys	Asp	Asn	Ile	Glu	Tyr	Leu	Asn	Ala	Asp	Glu	Asp
	9365					9370					9375			
His	Lys	Leu	Gln	Tyr	Asp	Tyr	Ala	Ile	Asn	Leu	Ala	Asn	Asn	Val
	9380					9385					9390			
Leu	Asp	Lys	Glu	Asn	Gly	Thr	Asn	Lys	Asp	Ala	Asn	Ile	Ile	Ile
	9395					9400					9405			
Gly	Met	Ile	Gln	Asn	Met	Asp	Asp	Ala	Arg	Ala	Leu	Leu	Asn	Gly
	9410					9415					9420			
Ile	Glu	Arg	Leu	Lys	Asp	Ala	Gln	Thr	Lys	Ala	His	Asn	Asp	Ile
	9425					9430					9435			
Lys	Asp	Thr	Leu	Lys	Arg	Gln	Leu	Asp	Glu	Ile	Glu	His	Ala	Asn
	9440					9445					9450			
Ala	Thr	Ser	Asn	Ser	Lys	Ala	Gln	Ala	Lys	Gln	Met	Val	Asn	Glu
	9455					9460					9465			

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Glu	Ala	Arg	Lys	Ala	Leu	Ser	Asn	Ile	Asn	Asp	Ala	Thr	Ser	Asn
	9470					9475					9480			
Asp	Leu	Val	Asn	Gln	Ala	Lys	Asp	Glu	Gly	Gln	Ser	Ala	Ile	Glu
	9485					9490					9495			
His	Ile	His	Ala	Asp	Glu	Leu	Pro	Lys	Ala	Lys	Leu	Asp	Ala	Asn
	9500					9505					9510			
Gln	Met	Ile	Asp	Gln	Lys	Val	Glu	Asp	Ile	Asn	His	Leu	Ile	Ser
	9515					9520					9525			
Gln	Asn	Pro	Asn	Leu	Ser	Asn	Glu	Glu	Lys	Asn	Lys	Leu	Ile	Ser
	9530					9535					9540			
Gln	Ile	Asn	Lys	Leu	Val	Asn	Gly	Ile	Lys	Asn	Glu	Ile	Gln	Gln
	9545					9550					9555			
Ala	Ile	Asn	Lys	Gln	Gln	Ile	Glu	Asn	Ala	Thr	Thr	Lys	Leu	Asp
	9560					9565					9570			
Glu	Val	Ile	Glu	Thr	Thr	Lys	Lys	Leu	Ile	Ile	Ala	Lys	Ala	Glu
	9575					9580					9585			
Ala	Lys	Gln	Met	Ile	Lys	Glu	Leu	Ser	Gln	Lys	Lys	Arg	Asp	Ala
	9590					9595					9600			
Ile	Asn	Asn	Asn	Thr	Asp	Leu	Thr	Pro	Ser	Gln	Lys	Ala	His	Ala
	9605					9610					9615			
Leu	Ala	Asp	Ile	Asp	Lys	Thr	Glu	Lys	Asp	Ala	Leu	Gln	His	Ile
	9620					9625					9630			
Glu	Asn	Ser	Asn	Ser	Ile	Asp	Asp	Ile	Asn	Asn	Asn	Lys	Glu	His
	9635					9640					9645			
Ala	Phe	Asn	Thr	Leu	Ala	His	Ile	Ile	Ile	Trp	Asp	Thr	Asp	Gln
	9650					9655					9660			

P07741US01_6-19-06_Sequence.txt

Gln	Pro	Leu	Val	Phe	Glu	Leu	Pro	Glu	Leu	Ser	Leu	Gln	Asn	Ala
	9665					9670					9675			
Leu	Val	Thr	Ser	Glu	Val	Val	Val	His	Arg	Asp	Glu	Thr	Ile	Ser
	9680					9685					9690			
Leu	Glu	Ser	Ile	Ile	Gly	Ala	Met	Thr	Leu	Thr	Asp	Glu	Leu	Lys
	9695					9700					9705			
Val	Asn	Ile	Val	Ser	Leu	Pro	Asn	Thr	Asp	Lys	Val	Ala	Asp	His
	9710					9715					9720			
Leu	Thr	Ala	Lys	Val	Lys	Val	Ile	Leu	Ala	Asp	Gly	Ser	Tyr	Val
	9725					9730					9735			
Thr	Val	Asn	Val	Pro	Val	Lys	Val	Val	Glu	Lys	Glu	Leu	Gln	Ile
	9740					9745					9750			
Ala	Lys	Lys	Asp	Ala	Ile	Lys	Thr	Ile	Asp	Val	Leu	Val	Lys	Gln
	9755					9760					9765			
Lys	Ile	Lys	Asp	Ile	Asp	Ser	Asn	Asn	Glu	Leu	Thr	Ser	Thr	Gln
	9770					9775					9780			
Arg	Glu	Asp	Ala	Lys	Ala	Glu	Ile	Glu	Arg	Leu	Lys	Lys	Gln	Ala
	9785					9790					9795			
Ile	Asp	Lys	Val	Asn	His	Ser	Lys	Ser	Ile	Lys	Asp	Ile	Glu	Thr
	9800					9805					9810			
Val	Lys	Arg	Thr	Asp	Phe	Glu	Glu	Ile	Asp	Gln	Phe	Asp	Pro	Lys
	9815					9820					9825			
Arg	Phe	Thr	Leu	Asn	Lys	Ala	Lys	Lys	Asp	Ile	Ile	Thr	Asp	Val
	9830					9835					9840			
Asn	Thr	Gln	Ile	Gln	Asn	Gly	Phe	Lys	Glu	Ile	Glu	Thr	Ile	Lys
	9845					9850					9855			

P07741US01_6-19-06_Sequence.txt

Gly	Leu	Thr	Ser	Asn	Glu	Lys	Thr	Gln	Phe	Asp	Lys	Gln	Leu	Thr
	9860					9865					9870			
Ala	Leu	Gln	Lys	Glu	Phe	Leu	Glu	Lys	Val	Glu	His	Ala	His	Asn
	9875					9880					9885			
Leu	Val	Glu	Leu	Asn	Gln	Leu	Gln	Gln	Glu	Phe	Asn	Asn	Arg	Tyr
	9890					9895					9900			
Lys	His	Ile	Leu	Asn	Gln	Ala	His	Leu	Leu	Gly	Glu	Lys	His	Ile
	9905					9910					9915			
Ala	Glu	His	Lys	Leu	Gly	Tyr	Val	Val	Val	Asn	Lys	Thr	Gln	Gln
	9920					9925					9930			
Ile	Leu	Asn	Asn	Gln	Ser	Ala	Ser	Tyr	Phe	Ile	Lys	Gln	Trp	Ala
	9935					9940					9945			
Leu	Asp	Arg	Ile	Lys	Gln	Ile	Gln	Leu	Glu	Thr	Met	Asn	Ser	Ile
	9950					9955					9960			
Arg	Gly	Ala	His	Thr	Val	Gln	Asp	Val	His	Lys	Ala	Leu	Leu	Gln
	9965					9970					9975			
Gly	Ile	Glu	Gln	Ile	Leu	Lys	Val	Asn	Val	Ser	Ile	Ile	Asn	Gln
	9980					9985					9990			
Ser	Phe	Asn	Asp	Ser	Leu	His	Asn	Phe	Asn	Tyr	Leu	His	Ser	Lys
	9995					10000					10005			
Phe	Asp	Ala	Arg	Leu	Arg	Glu	Lys	Asp	Val	Ala	Asn	His	Ile	Val
	10010					10015					10020			
Gln	Thr	Glu	Thr	Phe	Lys	Glu	Val	Leu	Lys	Gly	Thr	Gly	Val	Glu
	10025					10030					10035			
Pro	Gly	Lys	Ile	Asn	Lys	Glu	Thr	Gln	Gln	Pro	Lys	Leu	His	Lys
	10040					10045					10050			

P07741US01_6-19-06_Sequence.txt

Asn	Asp	Asn	Asp	Ser	Leu	Phe	Lys	His	Leu	Val	Asp	Asn	Phe	Gly
	10055					10060					10065			
Lys	Thr	Val	Gly	Val	Ile	Thr	Leu	Thr	Gly	Leu	Leu	Ser	Ser	Phe
	10070					10075					10080			
Trp	Leu	Val	Leu	Ala	Lys	Arg	Arg	Lys	Lys	Glu	Glu	Glu	Glu	Lys
	10085					10090					10095			
Gln	Ser	Ile	Lys	Asn	His	His	Lys	Asp	Ile	Arg	Leu	Ser	Asp	Thr
	10100					10105					10110			
Asp	Lys	Ile	Asp	Pro	Ile	Val	Ile	Thr	Lys	Arg	Lys	Ile	Asp	Lys
	10115					10120					10125			
Glu	Glu	Gln	Ile	Gln	Asn	Asp	Asp	Lys	His	Ser	Ile	Pro	Val	Ala
	10130					10135					10140			
Lys	His	Lys	Lys	Ser	Lys	Glu	Lys	Gln	Leu	Ser	Glu	Glu	Asp	Ile
	10145					10150					10155			
His	Ser	Ile	Pro	Val	Val	Lys	Arg	Lys	Gln	Asn	Ser	Asp	Asn	Lys
	10160					10165					10170			
Asp	Thr	Lys	Gln	Lys	Lys	Val	Thr	Ser	Lys	Lys	Lys	Lys	Thr	Pro
	10175					10180					10185			
Gln	Ser	Thr	Lys	Lys	Val	Val	Lys	Thr	Lys	Lys	Arg	Ser	Lys	Lys
	10190					10195					10200			

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 <212> PRT
 <213> Staphylococcus epidermidis

<400> 24

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P07741US01_6-19-06_Sequence.txt

Phe Ser Ile Arg Lys Tyr Gln Gly Tyr Gly Ala Thr Ser Val Ala Ile
 20 25 30

 Ile Gly Phe Ile Ile Ile Ser Cys Phe Ser Glu Ala Lys Ala Asp Ser
 35 40 45

 Asp Lys His Glu Ile Lys Ser His Gln Gln Ser Met Thr Asn His Leu
 50 55 60

 Thr Thr Leu Pro Ser Asp Asn Gln Glu Asn Thr Ser Asn Asn Glu Phe
 65 70 75 80

 Asn Asn Arg Asn His Asp Ile Ser His Leu Ser Leu Asn Lys Ser Ile
 85 90 95

 Gln Met Asp Glu Leu Lys Lys Leu Ile Lys Gln Tyr Lys Ala Ile Asn
 100 105 110

 Leu Asn Asp Lys Thr Glu Glu Ser Ile Lys Leu Phe Gln Ser Asp Leu
 115 120 125

 Val Gln Ala Glu Ser Leu Ile Asn Asn Pro Gln Ser Gln Gln His Val
 130 135 140

 Asp Ala Phe Tyr His Lys Phe Leu Asn Ser Ala Gly Lys Leu Arg Lys
 145 150 155 160

 Lys Glu Thr Val Ser Ile Lys His Glu Arg Ser Glu Ser Asn Thr Tyr
 165 170 175

 Arg Leu Gly Asp Glu Val Arg Ser Gln Thr Phe Ser His Ile Arg His
 180 185 190

 Lys Arg Asn Ala Val Ser Phe Arg Asn Ala Asp Gln Ser Asn Leu Ser
 195 200 205

 Thr Asp Pro Leu Lys Ala Asn Glu Ile Asn Pro Glu Ile Gln Asn Gly
 210 215 220

P07741US01_6-19-06_Sequence.txt

Asn Phe Ser Gln Val Ser Gly Gly Pro Leu Pro Thr Ser Ser Lys Arg
225 230 235 240

Leu Thr Val Val Thr Asn Val Asp Asn Trp His Ser Tyr Ser Thr Asp
245 250 255

Pro Asn Pro Glu Tyr Pro Met Phe Tyr Thr Thr Thr Ala Val Asn Tyr
260 265 270

Pro Asn Phe Met Ser Asn Gly Asn Ala Pro Tyr Gly Val Ile Leu Gly
275 280 285

Arg Thr Thr Asp Gly Trp Asn Arg Asn Val Ile Asp Ser Lys Val Ala
290 295 300

Gly Ile Tyr Gln Asp Ile Asp Val Val Pro Gly Ser Glu Leu Asn Val
305 310 315 320

Asn Phe Ile Ser Thr Ser Pro Val Phe Ser Asp Gly Ala Ala Gly Ala
325 330 335

Lys Leu Lys Ile Ser Asn Val Glu Gln Asn Arg Val Leu Phe Asp Ser
340 345 350

Arg Leu Asn Gly Met Gly Pro Tyr Pro Thr Gly Lys Leu Ser Ala Met
355 360 365

Val Asn Ile Pro Asn Asp Ile Asn Arg Val Arg Ile Ser Phe Leu Pro
370 375 380

Val Ser Ser Thr Gly Arg Val Ser Val Gln Arg Ser Ser Arg Glu His
385 390 395 400

Gly Phe Gly Asp Asn Ser Ser Tyr Tyr His Gly Gly Ser Val Ser Asp
405 410 415

Val Arg Ile Asn Ser Gly Ser Tyr Val Val Ser Lys Val Thr Gln Arg
420 425 430

P07741US01_6-19-06_Sequence.txt

Glu Tyr Thr Thr Arg Pro Asn Ser Ser Asn Asp Thr Phe Ala Arg Ala
435 440 445

Thr Ile Asn Leu Ser Val Glu Asn Lys Gly His Asn Gln Ser Lys Asp
450 455 460

Thr Tyr Tyr Glu Val Ile Leu Pro Gln Asn Ser Arg Leu Ile Ser Thr
465 470 475 480

Arg Gly Gly Ser Gly Asn Tyr Asn Asn Ala Thr Asn Lys Leu Ser Ile
485 490 495

Arg Leu Asp Asn Leu Asn Pro Gly Asp Arg Arg Asp Ile Ser Tyr Thr
500 505 510

Val Asp Phe Glu Ser Ser Ser Pro Lys Leu Ile Asn Leu Asn Ala His
515 520 525

Leu Leu Tyr Lys Thr Asn Ala Thr Phe Arg Gly Asn Asp Gly Gln Arg
530 535 540

Thr Gly Asp Asn Ile Val Asp Leu Gln Ser Ile Ala Leu Leu Met Asn
545 550 555 560

Lys Asp Val Leu Glu Thr Glu Leu Asn Glu Ile Asp Lys Phe Ile Arg
565 570 575

Asp Leu Asn Glu Ala Asp Phe Thr Ile Asp Ser Trp Ser Ala Leu Gln
580 585 590

Glu Lys Met Thr Glu Gly Gly Asn Ile Leu Asn Glu Gln Gln Asn Gln
595 600 605

Val Ala Leu Glu Asn Gln Ala Ser Gln Glu Thr Ile Asn Asn Val Thr
610 615 620

Gln Ser Leu Glu Ile Leu Lys Asn Asn Leu Lys Tyr Lys Thr Pro Ser
625 630 635 640

P07741US01_6-19-06_Sequence.txt

Gln Pro Ile Ile Lys Ser Asn Asn Gln Ile Pro Asn Ile Thr Ile Ser
645 650 655

Pro Ala Asp Lys Ala Asp Lys Leu Thr Ile Thr Tyr Gln Asn Thr Asp
660 665 670

Asn Glu Ser Ala Ser Ile Ile Gly Asn Lys Leu Asn Asn Gln Trp Ser
675 680 685

Leu Asn Asn Asn Ile Pro Gly Ile Glu Ile Asp Met Gln Thr Gly Leu
690 695 700

Val Thr Ile Asp Tyr Lys Ala Val Tyr Pro Glu Ser Val Val Gly Ala
705 710 715 720

Asn Asp Lys Thr Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr
725 730 735

Met Pro Arg Lys Glu Ala Thr Pro Leu Ser Pro Ile Val Glu Ala Asn
740 745 750

Glu Glu Arg Val Asn Val Val Ile Ala Pro Asn Gly Glu Ala Thr Gln
755 760 765

Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr Leu Val
770 775 780

Ala Ser Lys Asn Gly Ser Ser Trp Thr Leu Asn Lys Gln Ile Asp Tyr
785 790 795 800

Val Asn Ile Glu Glu Asn Ser Gly Lys Val Thr Ile Gly Tyr Gln Ala
805 810 815

Val Gln Pro Glu Ser Glu Val Ile Ala Thr Glu Thr Lys Gly Asn Ser
820 825 830

Asp Glu Ser Ala Glu Ser Arg Val Thr Met Pro Arg Lys Glu Ala Thr
835 840 845

P07741US01_6-19-06_Sequence.txt

Pro His Ser Pro Ile Val Glu Ala Asn Glu Glu His Val Asn Val Thr
850 855 860

Ile Ala Pro Asn Gly Glu Ala Thr Gln Ile Ala Ile Lys Tyr Arg Thr
865 870 875 880

Pro Asp Gly Gln Glu Thr Thr Leu Ile Ala Ser Lys Asn Gly Ser Ser
885 890 895

Trp Thr Leu Asn Lys Gln Ile Asp Tyr Val Asn Ile Glu Glu Asn Ser
900 905 910

Gly Lys Val Thr Ile Gly Tyr Gln Ala Val Gln Leu Glu Ser Glu Val
915 920 925

Ile Ala Thr Glu Thr Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg
930 935 940

Ile Thr Met Leu Arg Lys Glu Ala Thr Pro His Ser Pro Ile Val Glu
945 950 955 960

Ala Asn Glu Glu His Val Asn Val Thr Ile Ala Pro Asn Gly Glu Ala
965 970 975

Thr Gln Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr
980 985 990

Leu Val Ala Ser Lys Asn Glu Ser Ser Trp Thr Leu Asn Lys Gln Ile
995 1000 1005

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly
1010 1015 1020

Tyr Gln Ala Val Gln Pro Glu Ser Glu Ile Ile Ala Thr Glu Thr
1025 1030 1035

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr Met Pro
1040 1045 1050

P07741US01_6-19-06_Sequence.txt

Arg	Lys	Glu	Ala	Thr	Pro	Ile	Pro	Pro	Thr	Leu	Glu	Ala	Ser	Val
	1055					1060					1065			
Gln	Glu	Ala	Ser	Val	Thr	Val	Thr	Pro	Asn	Glu	Asn	Ala	Thr	Lys
	1070					1075					1080			
Val	Phe	Ile	Lys	Tyr	Leu	Asp	Ile	Asn	Asp	Glu	Ile	Ser	Thr	Ile
	1085					1090					1095			
Ile	Ala	Ser	Lys	Ile	Asn	Gln	Gln	Trp	Thr	Leu	Asn	Lys	Asp	Asn
	1100					1105					1110			
Phe	Gly	Ile	Lys	Ile	Asn	Pro	Leu	Thr	Gly	Lys	Val	Ile	Ile	Ser
	1115					1120					1125			
Tyr	Val	Ala	Val	Gln	Pro	Glu	Ser	Asp	Val	Ile	Ala	Ile	Glu	Ser
	1130					1135					1140			
Gln	Gly	Asn	Ser	Asp	Leu	Ser	Glu	Glu	Ser	Arg	Ile	Ile	Met	Pro
	1145					1150					1155			
Thr	Lys	Glu	Glu	Pro	Pro	Glu	Pro	Pro	Ile	Leu	Glu	Ser	Asp	Ser
	1160					1165					1170			
Ile	Glu	Ala	Lys	Val	Asn	Ile	Phe	Pro	Asn	Asp	Glu	Ala	Thr	Arg
	1175					1180					1185			
Ile	Val	Ile	Met	Tyr	Thr	Ser	Leu	Glu	Gly	Gln	Glu	Ala	Thr	Leu
	1190					1195					1200			
Val	Ala	Ser	Lys	Asn	Glu	Ser	Ser	Trp	Thr	Leu	Asn	Lys	Gln	Ile
	1205					1210					1215			
Asp	His	Val	Asn	Ile	Asp	Glu	Asn	Ser	Gly	Lys	Val	Thr	Ile	Gly
	1220					1225					1230			
Tyr	Gln	Ala	Val	Gln	Pro	Glu	Ser	Glu	Val	Ile	Ala	Thr	Glu	Thr
	1235					1240					1245			

p07741US01_6-19-06_Sequence.txt

Lys	Gly	Asn	Ser	Asp	Ala	Ser	Ala	Glu	Ser	Arg	Val	Thr	Met	Pro
	1250					1255					1260			
Arg	Lys	Glu	Ala	Thr	Pro	His	Ser	Pro	Ile	Val	Glu	Thr	Asn	Glu
	1265					1270					1275			
Glu	Arg	Val	Asn	Val	Val	Ile	Ala	Pro	Asn	Gly	Glu	Ala	Thr	Gln
	1280					1285					1290			
Ile	Ala	Ile	Lys	Tyr	Arg	Thr	Pro	Asp	Gly	Gln	Glu	Thr	Thr	Leu
	1295					1300					1305			
Ile	Ala	Ser	Lys	Asn	Gly	Ser	Ser	Trp	Thr	Leu	Asn	Lys	Gln	Ile
	1310					1315					1320			
Asp	His	Val	Asn	Ile	Asp	Glu	Asn	Ser	Gly	Lys	Val	Thr	Ile	Gly
	1325					1330					1335			
Tyr	Gln	Ala	Val	Gln	Pro	Glu	Ser	Glu	Ile	Ile	Ala	Thr	Glu	Thr
	1340					1345					1350			
Lys	Gly	Asn	Ser	Asp	Ala	Ser	Ala	Glu	Ser	Arg	Ile	Thr	Met	Pro
	1355					1360					1365			
Arg	Lys	Glu	Ala	Ile	Pro	His	Ser	Pro	Ile	Val	Glu	Ala	Asn	Glu
	1370					1375					1380			
Glu	His	Val	Asn	Val	Thr	Ile	Ala	Pro	Asn	Gly	Glu	Thr	Thr	Gln
	1385					1390					1395			
Ile	Ala	Val	Lys	Tyr	Arg	Thr	Pro	Asp	Gly	Gln	Glu	Ala	Thr	Leu
	1400					1405					1410			
Ile	Ala	Ser	Lys	Asn	Glu	Ser	Ser	Trp	Thr	Leu	Asn	Lys	Gln	Ile
	1415					1420					1425			
Asp	His	Val	Asn	Ile	Asp	Glu	Asn	Ser	Gly	Lys	Val	Thr	Ile	Gly
	1430					1435					1440			

p07741US01_6-19-06_Sequence.txt

Tyr	Gln	Ala	Val	Gln	Pro	Glu	Ser	Glu	Val	Ile	Ala	Thr	Glu	Thr
	1445					1450					1455			
Lys	Gly	Asn	Ser	Asp	Ala	Ser	Ala	Glu	Ser	Arg	Ile	Thr	Met	Pro
	1460					1465					1470			
Val	Lys	Glu	Lys	Thr	Pro	Ala	Pro	Pro	Ile	Ser	Ile	Ile	Asn	Glu
	1475					1480					1485			
Ser	Asn	Ala	Ser	Val	Glu	Ile	Ile	Pro	Gln	Val	Asn	Val	Thr	Gln
	1490					1495					1500			
Leu	Ser	Leu	Gln	Tyr	Ile	Asp	Ala	Lys	Gly	Gln	Gln	Gln	Asn	Leu
	1505					1510					1515			
Ile	Ala	Thr	Leu	Asn	Gln	Asn	Gln	Trp	Thr	Leu	Asn	Lys	Asn	Val
	1520					1525					1530			
Ser	His	Ile	Thr	Val	Asp	Lys	Asn	Thr	Gly	Lys	Val	Leu	Ile	Asn
	1535					1540					1545			
Tyr	Gln	Ala	Val	Tyr	Pro	Glu	Ser	Glu	Val	Ile	Ala	Arg	Glu	Ser
	1550					1555					1560			
Lys	Gly	Asn	Ser	Asp	Ser	Ser	Asn	Val	Ser	Met	Val	Ile	Met	Pro
	1565					1570					1575			
Arg	Lys	Thr	Ala	Thr	Pro	Lys	Pro	Pro	Ile	Ile	Lys	Val	Asp	Glu
	1580					1585					1590			
Met	Asn	Ala	Ser	Leu	Ala	Ile	Ile	Pro	Tyr	Lys	Asn	Asn	Thr	Ala
	1595					1600					1605			
Ile	Asn	Ile	His	Tyr	Ile	Asp	Lys	Lys	Gly	Ile	Lys	Ser	Met	Val
	1610					1615					1620			
Thr	Ala	Ile	Lys	Asn	Asn	Asp	Gln	Trp	Gln	Leu	Asp	Glu	Lys	Ile
	1625					1630					1635			

P07741US01_6-19-06_Sequence.txt

Lys	Tyr	Val	Lys	Ile	Asp	Ala	Lys	Thr	Gly	Thr	Val	Ile	Ile	Asn
1640						1645					1650			
Tyr	Gln	Ile	Val	Gln	Glu	Asn	Ser	Glu	Ile	Ile	Ala	Thr	Ala	Ile
1655						1660					1665			
Asn	Gly	Asn	Ser	Asp	Lys	Ser	Glu	Glu	Val	Lys	Val	Leu	Met	Pro
1670						1675					1680			
Ile	Lys	Glu	Phe	Thr	Pro	Leu	Ala	Pro	Leu	Leu	Glu	Thr	Asn	Tyr
1685						1690					1695			
Lys	Lys	Ala	Thr	Val	Ser	Ile	Leu	Pro	Gln	Ser	Asn	Ala	Thr	Lys
1700						1705					1710			
Leu	Asp	Phe	Lys	Tyr	Arg	Asp	Lys	Lys	Gly	Asp	Ser	Lys	Ile	Ile
1715						1720					1725			
Ile	Val	Lys	Arg	Phe	Lys	Asn	Ile	Trp	Lys	Ala	Asn	Glu	Gln	Ile
1730						1735					1740			
Ser	Gly	Val	Thr	Ile	Asn	Pro	Glu	Phe	Gly	Gln	Val	Val	Ile	Asn
1745						1750					1755			
Tyr	Gln	Ala	Val	Tyr	Pro	Glu	Ser	Asp	Ile	Leu	Ala	Ala	Gln	Tyr
1760						1765					1770			
Val	Gly	Asn	Ser	Asp	Ala	Ser	Glu	Trp	Ala	Lys	Val	Lys	Met	Pro
1775						1780					1785			
Lys	Lys	Glu	Leu	Ala	Pro	His	Ser	Pro	Ser	Leu	Ile	Tyr	Asp	Asn
1790						1795					1800			
Arg	Asn	Asn	Lys	Ile	Leu	Ile	Ala	Pro	Asn	Ser	Asn	Ala	Thr	Glu
1805						1810					1815			
Met	Glu	Leu	Ser	Tyr	Val	Asp	Lys	Asn	Asn	Gln	Ser	Leu	Lys	Val
1820						1825					1830			

p07741US01_6-19-06_Sequence.txt

Lys Ala Leu Lys Ile Asn Asn Arg Trp Lys Phe Asp Ser Ser Val
1835 1840 1845

Ser Asn Ile Ser Ile Asn Pro Asn Thr Gly Lys Ile Val Leu Gln
1850 1855 1860

Pro Gln Phe Leu Leu Thr Asn Ser Lys Ile Ile Val Phe Ala Lys
1865 1870 1875

Lys Gly Asn Ser Asp Ala Ser Ile Ser Val Ser Leu Arg Val Pro
1880 1885 1890

Ala Val Lys Lys Ile Glu Leu Glu Pro Met Phe Asn Val Pro Val
1895 1900 1905

Leu Val Ser Leu Asn Lys Lys Arg Ile Gln Phe Asp Asp Cys Ser
1910 1915 1920

Gly Val Lys Asn Cys Leu Asn Lys Gln Ile Ser Lys Thr Gln Leu
1925 1930 1935

Pro Asp Thr Gly Tyr Ser Asp Lys Ala Ser Lys Ser Asn Ile Leu
1940 1945 1950

Ser Val Leu Leu Leu Gly Phe Gly Phe Leu Ser Tyr Ser Arg Lys
1955 1960 1965

Arg Lys Glu Lys Gln
1970

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<211> 10
<212> PRT
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<220>
<221> misc_feature
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<223> Xaa can be any naturally occurring amino acid

<400> 25

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1 5 10

<210> 26

<211> 30

<212> DNA

<213> Enterococcus faecalis

<400> 26

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30

<210> 27

<211> 33

<212> DNA

<213> Enterococcus faecalis

<400> 27

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33

<210> 28

<211> 30

<212> DNA

<213> Enterococcus faecalis

<400> 28

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30

<210> 29

<211> 33

<212> DNA

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33

<210> 30

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<212> DNA

<213> Enterococcus faecalis

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33

<210> 31
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<213> Enterococcus faecalis

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33

<210> 32
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<213> Enterococcus faecalis

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28

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<400> 33
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31

<210> 34
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33

<210> 35
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<212> DNA
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36

<210> 36
<211> 27
<212> DNA
<213> Enterococcus faecalis

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